

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2001, 14:04:33 ; Search time 2493.36 Seconds
(without alignments)
11056.979 Million cell updates/sec

Title: US-09-524-101-1
Perfect score: 1573
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 17159718 seqs, 8763200856 residues

Total number of hits satisfying chosen parameters: 34319436

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1573	100.0	1573	1	PCT-US00-06602A-1	Sequence 1, Appli
3	1573	100.0	1573	16	US-09-268-969-1	Sequence 1, Appli
4	1573	100.0	1573	19	US-09-524-101-1	Sequence 1, Appli
5	1230	78.2	1241	49	US-60-167-217-22997	Sequence 22997, A
6	1230	78.2	1241	50	US-60-171-625-449	Sequence 449, App
7	1230	78.2	1241	50	US-60-173-464-18652	Sequence 18652, A
8	1230	78.2	1241	52	US-60-191-637-22729	Sequence 22729, A
9	1230	78.2	1241	52	US-60-191-681-17941	Sequence 17941, A
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15	1067	67.8	8805	16	US-09-268-969-7	Sequence 7, Appli
16	1067	67.8	27425	1	PCT-US00-06602-18	Sequence 18, Appli
17	1067	67.8	27425	1	PCT-US00-06602A-18	Sequence 18, Appli
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21	83	5.3	1497	16	US-09-270-767-13214	Sequence 2570, Ap
22	48.2	3.1	15822	24	US-09-620-392-2570	Sequence 4686, Ap
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45 38.2 2.4 1539 16 US-09-252-991A-2452 Sequence 2452, Ap

ALIGNMENTS

RESULT 1
PCT-US00-06602-1
; Sequence 1, Application PC/TUS00006602
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences
; CURRENT APPLICATION NUMBER: PCT/US00/06602
; CURRENT FILING DATE: 2000-03-15
; EARLIER APPLICATION NUMBER: EX99-001
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
PCT-US00-06602-1

Query Match 100.0%; Score 1573; DB 1; Length 1573;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 1, Application PC/TUS00006602A
; GENERAL INFORMATION:

APPLICANT: EXELIXIS, INC
TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
FILE REFERENCE: Insect p53 sequences
CURRENT APPLICATION NUMBER: PCT/US00/06602A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: EX99-001
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1573
TYPE: DNA
ORGANISM: Drosophila melanogaster
PCT-US00-06602A-1

Query Match 100.0%; Score 1573; DB 1; Length 1573;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1561 tcatatatttgcac 1573

RESULT 3
US-09-268-969-1
; Sequence 1, Application US/09268969
; GENERAL INFORMATION:
; APPLICANT: Buchman, Andrew R.
; APPLICANT: Platt, Darren M.
; APPLICANT: Ollmann, Michael M.
; APPLICANT: Young, Lynn M.
; APPLICANT: Damsky, Madelyn R.
; APPLICANT: Keegan, Kevin P.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER TUMOR
; FILE REFERENCE: 7326-084
; CURRENT APPLICATION NUMBER: US/09/268,969
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0


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; SEQ ID NO 1
;
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112)..(1256)
US-09-268-969-1

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Query Match	100.0%;	Score 1573;	DB 16;	Length 1573;
Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 1573:	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY	1	aaatccaaatagtcggtggcactacgattctgtagtctttttagcggaattttaaat	60
Db	1	aaatccaaatagtcggtggcactacgattctgtagtctttttagcggaattttaaat	60
QY	61	atttagcctcttcccccaacaagatcgcttgatcacatatagccgactaagatgtatata	120
Db	61	atttagcctcttcccccaacaagatcgcttgatcacatatagccgactaagatgtatata	120
QY	121	tcacagccaatgtcgtggcacaaaagaagcactgatccgaggatgactccacggaggtc	180
Db	121	tcacagccaatgtcgtggcacaaaagaagcactgatccgaggatgactccacggaggtc	180
QY	181	gataccaaggaggatattccgaaaaacggtggaggtatcggggtatcgggaattgaccacggaa	240
Db	181	gataccaaggaggatattccgaaaaacggtggaggtatcggggtatcgggaattgaccacggaa	240
QY	241	cccattgccttcttgcagggtattaaacctcgggaattctgatcgagttcagccagcaatcc	300
Db	241	cccattgccttcttgcagggtattaaacctcgggaattctgatcgagttcagccagcaatcc	300
QY	301	gtctgcgcgaaatgatgctgcaggacattcagatccaggcgaacacgctg_aagcta	360
Db	301	gtctgcgcgaaatgatgctgcaggacattcagatccaggcgaacacgctg_c.aagcta	360
QY	361	gagaatcacacaatcggtggttatgtcttcagcatggtctctggatgagccgccaaagtct	420
Db	361	gagaatcacacaatcggtggttatgtcttcagcatggtctctggatgagccgccaaagtct	420
QY	421	ctttggatgtactcgattccgctgaacaagctctacatccggatgaacaaggcccttcaac	480
Db	421	ctttggatgtactcgattccgctgaacaagctctacatccggatgaacaaggcccttcaac	480
QY	481	gtggacgttcagttcgaattcgaatgtcccatcccaaccacttaatttcggtgtgttcctt	540
Db	481	gtggacgttcagttcgaattcgaatgtcccatcccaaccactt.cttctggtgtgttcctt	540
QY	541	tgccttccaaatgatgtgagtgctcccggtggtccgctgtcgaataaaccttagcgttgag	600
Db	541	tgccttccaaatgatgtgagtgctcccggtggtccgctgtcgaataaaccttagcgttgag	600
QY	601	cctttgacggccaaataacgcgaataatgcgcgagagcttgctgcgcagcgagaatcccaa	660
Db	601	cctttgacggccaaataacgcgaataatgcgcgagagcttgctgcgcagcgagaatcccaa	660
QY	661	agtgatatattgtggaaatgctcaggggcaaggggaatttccgagcgttttccggttgtagtc	720
Db	661	agtgatatattgtggaaatgctcaggggcaaggggaatttccgagcgttttccggttgtagtc	720
QY	721	cccctgaacatgagccggtctgttaaccgcgcagtggggtcacgcgcgaaccctt_cccttc	780
Db	721	cccctgaacatgagccggtctgttaaccgcgcagtggggtcacgcgcgcgaaccctt_ggccttc	780
QY	781	aagttcgtctgccaaaactcgtgtatcggggcgaaaaaagaacttcccttagtctctcgcctg	840
Db	781	aagttcgtctgccaaaactcgtgtatcggggcgaaaaaagaactt.ccttagtctctcgcctg	840
QY	841	gagaaagcatgcggcgatatcgtgggaacagcatgtttatacatgtttaaaalatgtacgtgc	900
Db	841	gagaaagcatgcggcgatatcgtgggaacagcatgtttatacatgtttaaaalatgtacgtgc	900

Query Match 100.0%; Score 1573; DB 19; Length 1573;

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RESULT      4
US-09-524-101-1
; Sequence 1, Application US/09524101
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: insect p53 EX00-015
; CURRENT APPLICATION NUMBER: US/09/524,101
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 09/268,969
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/184,373
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-524-101-1

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Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 1573; Conservative 0;

QY 1 aaatccaaatagtcggtgcccactacgattctgtagtttttttagcgaattttta 60
Db 1 aaatccaaatagtcggtgcccactacgattctgtagtttttttagcgaattttta 60

QY 61 atttagcctctctcccaacaagaatgcgttgatcagatatagcactaaagtatatata 120
Db 61 atttagcctctctcccaacaagaatgcgttgatcagatatagcactaaagtatatata 120

QY 121 tcaagcccaatgtcgtgycacaaagaagaacgactgattcccgagcactccacggaggtc 180
Db 121 tcaagcccaatgtcgtgycacaaagaagaacgactgattcccgagcactccacggaggtc 180

QY 181 gatataagaggaggtattccgaaaacggtgaggtatcgggagtcgggaattgaccacggaa 240
Db 181 gatataagaggaggtattccgaaaacggtgaggtatcgggagtcgggaattgaccacggaa 240

QY 241 cccatgcccctcttcgagggattaaactccgggaatctgatgcagttcagccagcaatcc 300
Db 241 cccatgcccctcttcgagggattaaactccgggaatctgatgcagttcagccagcaatcc 300

QY 301 gtgctgcgcgaaatgatgctgcaggaacattcagatccaggcgcacagctgcccagacta 360
Db 301 gtgctgcgcgaaatgatgctgcaggaacattcagatccaggcgcacagctgcccagacta 360

QY 361 gagaatcacaaacatcgtggttattgctcttcagcaggttctggtgagcgcgcgaagctc 420
Db 361 gagaatcacaaacatcgtggttattgctcttcagcaggttctggtgagcgcgcgaagctc 420

QY 421 ctttggatgtactcagttccgctgaacaaagctctacatccggatgaaacaggccttcaac 480
Db 421 ctttggatgtactcagttccgctgaacaaagctctacatccggatgaaacaggccttcaac 480

QY 481 gtggacgttcagttcagttcctaaatgcccacccatccaccacttaatttgcgtgttccct 540
Db 481 gtggacgttcagttcagttcctaaatgcccacccatccaccacttaatttgcgtgttccct 540

QY 541 tgccttcccaatgatgtagtgctcccggtggtccgctgtcacaacacacttagcgttag 600
Db 541 tgccttcccaatgatgtagtgctcccggtggtccgctgtcacaacacacttagcgttag 600

QY 601 cctttgacggcccaataacgcgcaaaaatgcgcgagagcttgcgcgagcagagaatcccaac 660
Db 601 cctttgacggcccaataacgcgcaaaaatgcgcgagagcttgcgcgagcagagaatcccaac 660

QY 661 agtgtatatgtggaatgctcagggcgaagggaattcccgagcgttttccggttagtc 720
Db 661 agtgtatatgtggaatgctcagggcgaagggaattcccgagcgttttccggttagtc 720

QY 721 cccctgaacatgagccgtctgttaaccgcagtggtggtcagcgcagaccctgaccttc 780
Db 721 cccctgaacatgagccgtctgttaaccgcagtggtggtcagcgcagaccctgaccttc 780

QY 781 aagttcgtctgcccactcgtgtatcggggcgaagaaacttcccttagtcttctgacctg 840
Db 781 aagttcgtctgcccactcgtgtatcggggcgaagaaacttcccttagtcttctgacctg 840

QY 841 gagaaagcatgcggcgatatcgtgggacagcatgtttatcatgitaataatgtacgtgc 900
Db 841 gagaaagcatgcggcgatatcgtgggacagcatgtttatcatgitaataatgtacgtgc 900

QY 901 cccaaagcgggcatccaaagacgaacccagctcaatagcaagaagcgcgaagtcggtg 960
Db 901 cccaaagcgggcatccaaagacgaacccagctcaatagcaagaagcgcgaagtcggtg 960

QY 961 ccggaagccgcgaagaagatgagccgttccaaagtgctcgggtgcattgctataaaagacg 1020
Db 961 ccggaagccgcgaagaagatgagccgttccaaagtgctcgggtgcattgctataaaagacg 1020

QY 1021 gaggacacggagagcaatgatagccgagactgcgacgactcccgagagtggaacgtg 1080
Db 1021 gaggacacggagagcaatgatagccgagactgcgacgactcccgagagtggaacgtg 1080

Db 1021 gaggacacggagagcaatgatagccgagactgcgacgactcccgagagtggaacgtg 1080
QY 1081 tcgcggacacccggtggtgattaccgtctgctattacgtgcccccaataaaggaatggctg 1140
Db 1081 tcgcggacacccggtggtgattaccgtctgctattacgtgcccccaataaaggaatggctg 1140
QY 1141 ctgcagagcatcgcgggcatgattaaaggagcgcgcggtggaagtcctgcgcaatcccaac 1200
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QY 1201 caagagaatctacgtgcgcacatgcacaataattgtagccttaagaaacgtgactacgag 1260
Db 1201 caagagaatctacgtgcgcacatgcacaataattgtagccttaagaaacgtgactacgag 1260
QY 1261 ctgcatgactctctgactggtgcacaatctccaggtatcagatacctttgaaatgtgt 1320
Db 1261 ctgcatgactctctgactggtgcacaatctccaggtatcagatacctttgaaatgtgt 1320
QY 1321 tgcactgtgggtatactacatacgtattagttatcttaagtgttagttagtctgttgc 1380
Db 1321 tgcactgtgggtatactacatacgtattagttatcttaagtgttagttagtctgttgc 1380
QY 1381 gtaaggcgtttaacggtgatattccctcttttggcatgttcgatggccgaaaaaacaacat 1440
Db 1381 gtaaggcgtttaacggtgatattccctcttttggcatgttcgatggccgaaaaaacaacat 1440
QY 1441 ttttatattttgatagtatatactgtgttaactgactgtctatgtgactacgttaactttt 1500
Db 1441 ttttatattttgatagtatatactgtgttaactgactgtctatgtgactacgttaactttt 1500
QY 1501 gtctaccacaacaaacatactctgtacaaaaaaggccaaaagtgaatttattaaagagttg 1560
Db 1501 gtctaccacaacaaacatactctgtacaaaaaaggccaaaagtgaatttattaaagagttg 1560
QY 1561 tcataattttgcaa 1573
Db 1561 tcataattttgcaa 1573

RESULT 5
US-60-167-217-22997
; Sequence 22997, Application US/60167217
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000152
; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22997
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: Drosophila
US-60-167-217-22997

Query Match 78.2%; Score 1230; DB 49; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 gtggccactacgattctgtagtttttttttagcgaatttttaatttagcctctctccc 76
Db 1 gtggccactacgattctgtagtttttttttagcgaatttttaatttagcctctctccc 60

QY 77 caacaagatcgttgatcagatatagccgactaagatgtatatataacagccaatgtcgt 136
Db 61 caacaagatcgttgatcagatatagccgactaagatgtatatataacagccaatgtcgt 120

QY 137 ggcacaaaagaagcactgattccggaggtactccagcaggtcgcagatatcaaggaggata 196
Db 137 ggcacaaaagaagcactgattccggaggtactccagcaggtcgcagatatcaaggaggata 196

Db 121 ggcacaaagacactgattccgaggatgactccacggaggctgatatacaaggaggata 180
QY 197 ttccgaaaaacggtgaggatcgaggatcggaattgaccacgggaacccatggccttctgc 256
Db 181 ttccgaaaaacggtgaggatcgaggatcggaattgaccacgggaacccatggccttctgc 240
QY 257 agggattaaactccgggaatctgatgcagtttcagccagcaatcgtgctgcgcgaaatga 316
Db 241 agggattaaactccgggaatctgatgcagtttcagccagcaatcgtgctgcgcgaaatga 300
QY 317 tgcgcaggacattcagatccaggcgaaacacgcctgccccagctagagaatcaacaacatcg 376
Db 301 tgcgcaggacattcagatccaggcgaaacacgcctgccccagctagagaatcaacaacatcg 360
QY 377 gtggttattgtctcagcatggttctggatgagcccgcccaagtctt tttgagtgtactoga 436
Db 361 gtggttattgtctcagcatggttctggatgagcccgcccaagtctt tttgagtgtactoga 420
QY 437 ttccgctgaacaaactctacatccggatgaacaaaggccttcacgtggagcttcagttca 496
Db 421 ttccgctgaacaaactctacatccggatgaacaaaggccttcacgtggagcttcagttca 480
QY 497 agtctaaaaatgcccatcccaacacctaatttgcgtgtgtcttcttgccttcccaatgatg 556
Db 481 agtctaaaaatgcccatcccaacacctaatttgcgtgtgtcttcttgccttcccaatgatg 540
QY 557 tgaagtctcccggtgtccgctgtcaaaaaatcaccttagcgtttgagccttttgacggccaata 616
Db 541 tgaagtctcccggtgtccgctgtcaaaaaatcaccttagcgtttgagccttttgacggccaata 600
QY 617 acgcaaaaaatgcgcgagagccttgcgcgacgagagaatcccaacagtgatatattgtggaa 676
Db 601 acgcaaaaaatgcgcgagagccttgcgcgacgagagaatcccaacagtgatatattgtggaa 660
QY 677 atgctcaggggcaaggaaatttccgagcgttttccggtttagtccctgaacatgagcc 736
Db 661 atgctcaggggcaaggaaatttccgagcgttttccggtttagtccctgaacatgagcc 720
QY 737 ggtctgaaccccgagtggtcgcgcgacgacccctggccttcaagtctgtctgccaaa 796
Db 721 ggtctgaaccccgagtggtcgcgcgacgacccctggccttcaagtctgtctgccaaa 780
QY 797 actcgtgtatcgggcgaaaaaagaaacttcccttagtcttctgcctggagaaagcatgcggcg 856
Db 781 actcgtgtatcgggcgaaaaaagaaacttcccttagtcttctgcctggagaaagcatgcggcg 840
QY 857 atatcgtgggacagcatgtttatatacatgtttaaaatattgtacgtgcccccaagcggatcgca 916
Db 841 atatcgtgggacagcatgtttatatacatgtttaaaatattgtacgtgcccccaagcggatcgca 900
QY 917 tccaagacgaacccagcctcaatagcaagaagcgcaagtcctgcccggaaagccgcgaag 976
Db 901 tccaagacgaacccagcctcaatagcaagaagcgcaagtcctgcccggaaagccgcgaag 960
QY 977 aagatgagccgtcccaagggtgcgtcgtgcatgtctataaagacggaggaacacggagagca 1036
Db 961 aagatgagccgtcccaagggtgcgtcgtgcatgtctataaagacgaggacacggagagca 1020
QY 1037 atgatagccgagactgcgacgactccgcgcagagtggaacgttgcgcggacacgggatg 1096
Db 1021 atgatagccgagactgcgacgactccgcgcagagtggaacgttgcgcggacacgggatg 1080
QY 1097 gcgattacgctctggtattacgtgcccccaataaaggaatggctgtgcagagcatcgagg 1156
Db 1081 gcgattacgctctggtattacgtgcccccaataaaggaatggctgtgcagagcatcgagg 1140
QY 1157 gcatgattaaggagggcggtggaagtccctgcgcaatcccaacaaagagaatctacgtc 1216
Db 1141 gcatgattaaggagggcggtggaagtccctgcgcaatcccaacaaagagaatctacgtc 1200
QY 1217 gccatgccacaacaaattgctgagcccttaaga 1246
Db 1201 gccatgccacaacaaattgctgagcccttaaga 1230

RESULT 6
US-60-171-625-449
; Sequence 449, Application US/60171625
; GENERAL INFORMATION:
; APPLICANT: Skupski, Marian
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS THAT SHOW
; TITLE OF INVENTION: HIGH HOMOLOGU TO KNOWN HUMAN DISEASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000179
; CURRENT APPLICATION NUMBER: US/60/171,625
; CURRENT FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-171-625-449

Query Match 78.2%; Score 1230; DB 50; Length 241;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 gtggccactacgattctgtagttttttgttagcgaatttttaatatatttagcctctccc 76
Db 1 gtggccactacgattctgtagttttttgttagcgaatttttaatatatttagcctctccc 60
QY 77 caacaagatcgttggatcagatatagccgactaagatgtatatatacacagccaatgtcgt 136
Db 61 caacaagatcgttggatcagatatagccgactaagatgtatatatacacagccaatgtcgt 120
QY 137 ggcacaaagaaagcaactgattccgaggatgactccacggaggtcgatatcaaggaggata 196
Db 121 ggcacaaagaaagcaactgattccgaggatgactccacggaggtcgatatcaaggaggata 180
QY 197 ttccgaaaaacggtgagggtatcggtatcggaattgaccacgggaacccatggccttctgc 256
Db 181 ttccgaaaaacggtgagggtatcggtatcggaattgaccacgggaacccatggccttctgc 240
QY 257 agggattaaactccgggaatctgatgcagttccagcagcaatccgtgctgcgcgaaatga 316
Db 241 agggattaaactccgggaatctgatgcagttccagcagcaatccgtgctgcgcgaaatga 300
QY 317 tgcgcaggacattcagatccaggcgaaacacgcctgccccagctagagaatcaacaacatcg 376
Db 301 tgcgcaggacattcagatccaggcgaaacacgcctgccccagctagagaatcaacaacatcg 360
QY 377 gtggttattgtctcagcatggttctggatgagcccgcccaagtctt tttgagtgtactoga 436
Db 361 gtggttattgtctcagcatggttctggatgagcccgcccaagtctt tttgagtgtactoga 420
QY 437 ttccgctgaacaaactctacatccggatgaacaaaggccttcacgtggagcttcagttca 496
Db 421 ttccgctgaacaaactctacatccggatgaacaaaggccttcacgtggagcttcagttca 480
QY 497 agtctaaaaatgcccatcccaacacctaatttgcgtgtgtcttcttgccttcccaatgatg 556
Db 481 agtctaaaaatgcccatcccaacacctaatttgcgtgtgtcttcttgccttcccaatgatg 540
QY 557 tgaagtctcccggtgtccgctgtcaaaaaatcaccttagcgtttgagccttttgacggccaata 616
Db 541 tgaagtctcccggtgtccgctgtcaaaaaatcaccttagcgtttgagccttttgacggccaata 600
QY 617 acgcaaaaaatgcgcgagagccttgcgcgacgagagaatcccaacagtgatatattgtggaa 676
Db 601 acgcaaaaaatgcgcgagagccttgcgcgacgagagaatcccaacagtgatatattgtggaa 660
QY 677 atgctcaggggcaaggaaatttccgagcgttttccggtttagtccctgaacatgagcc 736
Db 661 atgctcaggggcaaggaaatttccgagcgttttccggtttagtccctgaacatgagcc 720

RESULT 8
US-60-191-637-22729
; Sequence 22729, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 42660
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22729
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-637-22729

Query Match 78.2%; Score 1230; DB 52; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 gtggccactacgattctgttagttttttgttagcgaaatttttaatttagcctctccc 76
Db 1 gtggccactacgattctgttagttttttgttagcgaaatttttaatttagcctctccc 60

QY 77 caacaagatcgcttgatcagatatagccgactaagatgtatatatcacagccaattgcgt 136
Db 61 caacaagatcgcttgatcagatatagccgactaagatgtatatatcacagccaattgcgt 120

QY 137 ggcacaaaagaagcactgattccgaggaatgactccagagggtcgatatcaaggaggata 196
Db 121 ggcacaaaagaagcactgattccgaggaatgactccagagggtcgatatcaaggaggata 180

QY 197 ttccgaaaacggtggaggtatcggtatcggaattgacacaggaacccatggcctcttgc 256
Db 181 ttccgaaaacggtggaggtatcggtatcggaattgacacaggaacccatggcctcttgc 240

QY 257 agggattaaactccgggaattctgatgcagttcagccagcaaatccgtgctgcgcgaatga 316
Db 241 agggattaaactccgggaattctgatgcagttcagccagcaaatccgtgctgcgcgaatga 300

QY 317 tgcgtcaggacattcagatccagcggaacacgctgcccagctagagaatcacacacatcg 376
Db 301 tgcgtcaggacattcagatccagcggaacacgctgcccagctagagaatcacacacatcg 360

QY 377 gtggttattgttcagcatggttctggtatgagccgcccagctctttggtgactcga 436
Db 361 gtggttattgttcagcatggttctggtatgagccgcccagctctttggtgactcga 420

QY 437 ttccgctgaacaaagctctacatccgggatgaacaaaggccttcaacgtggacgttcaagttca 496
Db 421 ttccgctgaacaaagctctacatccgggatgaacaaaggccttcaacgtggacgttcaagttca 480

QY 497 agtctaaaatgcccatcccaacttaatttgcgtgtgttctcttgccttcccaatgatg 556
Db 481 agtctaaaatgcccatcccaacttaatttgcgtgtgttctcttgccttcccaatgatg 540

QY 557 tgagtgtccctggtccgctgtcaaaaatccacttagcgttgagcctttgacggccaata 616
Db 541 tgagtgtccctggtccgctgtcaaaaatccacttagcgttgagcctttgacggccaata 600

QY 617 acgcaaaaaatgcgcgagagcttgctgcgcagcgagaaatcccaacagtgatatattgtggaa 676
Db 601 acgcaaaaaatgcgcgagagcttgctgcgcagcgagaaatcccaacagtgatatattgtggaa 660

QY 677 atgctcagggcaagggaatttccgagcgttttccgtttagtccccctgaacatgagcc 736
Db 661 atgctcagggcaagggaatttccgagcgttttccgtttagtccccctgaacatgagcc 720

QY 737 ggtctgtaaccgcgcagtggtctcaagcgcgcagaccctggcctcaagttcgtctgcca 796
Db 721 ggtctgtaaccgcgcagtggtctcaagcgcgcagaccctggcctcaagttcgtctgcca 780

QY 797 actcgtgatatcgcggaagaaacttcccttagttcttctgctggagagaaagcgcgcg 856
Db 781 actcgtgatatcgcggaagaaacttcccttagttcttctgctggagagaaagcgcgcg 840

QY 857 atatcgtgggacagcatgttatatacatgtttaaaatatgtacgtgcccccaagcgggatcgca 916
Db 841 atatcgtgggacagcatgttatatacatgtttaaaatatgtacgtgcccccaagcgggatcgca 900

QY 917 tccaagaacgaacgcagctcaatagcaagaagcgaagtcggtccgggaagcgcgcgaag 976
Db 901 tccaagaacgaacgcagctcaatagcaagaagcgaagtcggtccgggaagcgcgcgaag 960

QY 977 aagatgagccgtccaaaggtgcgtgcgtgcatgtctataaagacggaggaacagagagca 1036
Db 961 aagatgagccgtccaaaggtgcgtgcgtgcatgtctataaagacggaggaacagagagca 1020

QY 1037 atgataccgagactgcgacgactccgcgcgcagagtggaacgtgctgcggacacccggtg 1096
Db 1021 atgataccgagactgcgacgactccgcgcgcagagtggaacgtgctgcggacacccggtg 1080

QY 1097 gcgattaccgtctggtctattacgtgcccccaataaagaatggtgctgcagagcgcgcg 1156
Db 1081 gcgattaccgtctggtctattacgtgcccccaataaagaatggtgctgcagagcgcgcg 1140

QY 1157 gcatgattaaaggagcgcggtggaagtcgctgcgaatcccaacaaagagaatctacgtc 1216
Db 1141 gcatgattaaaggagcgcggtggaagtcgctgcgaatcccaacaaagagaatctacgtc 1200

QY 1217 gccatgccaacaaattgctgagccttaaga 1246
Db 1201 gccatgccaacaaattgctgagccttaaga 1230

RESULT 9
US-60-191-681-17941
; Sequence 17941, Application US/60191681
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
; TITLE OF INVENTION: USES THEREOF.
; FILE REFERENCE: CL000390
; CURRENT APPLICATION NUMBER: US/60/191,681
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 30973
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17941
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-681-17941

Query Match 78.2%; Score 1230; DB 52; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 gtggccactacgattctgttagttttttgttagcgaaatttttaatttagcctctccc 76
Db 1 gtggccactacgattctgttagttttttgttagcgaaatttttaatttagcctctccc 60

QY 77 caacaagatcgcttgatcagatatagccgactaagatgtatatatcacagccaattgcgt 136
Db 61 caacaagatcgcttgatcagatatagccgactaagatgtatatatcacagccaattgcgt 120

QY 137 ggcacaaaagaagcactgattccgaggaatgactccagagggtcgatatcaaggaggata 196
Db 121 ggcacaaaagaagcactgattccgaggaatgactccagagggtcgatatcaaggaggata 180

QY 197 ttccgaaaacggtgaggtatcgggatacgggaattgaccacggaacccatggccttctgc 256
Db 181 ttccgaaaacggtgaggtatcgggatacgggaattgaccacggaacccatggccttctgc 240
QY 257 agggattaaactccgggaatctgatgcagttcagccagcaatccgtgctgcggaatga 316
Db 241 agggattaaactccgggaatctgatgcagttcagccagcaatccgtgctgcggaatga 300
QY 317 tgctgcaggacattcagatccaggcgaacacgcgtcccaagctagagaaatcaacaatcg 376
Db 301 tgctgcaggacattcagatccaggcgaacacgcgtcccaagctagagaaatcaacaatcg 360
QY 377 gtggttattgcttcagcatggttctggtatgagccgcccagttcttttggtactcga 436
Db 361 gtggttattgcttcagcatggttctggtatgagccgcccagttcttttggtactcga 420
QY 437 ttccgctgaacaagctctacatccgggatgaacaaggccttcaacgtggacgttcaattca 496
Db 421 ttccgctgaacaagctctacatccgggatgaacaaggccttcaacgtggacgttcaattca 480
QY 497 agtctaaaatgcccatcccaaccacttaatttgctggtgttcttcttcccaatgatg 556
Db 481 agtctaaaatgcccatcccaaccacttaatttgctggtgttcttcttcccaatgatg 540
QY 557 tgagtgtcccggtgctgcgctgtcaaaaatcaccttagcgttgagcccttgacggccaata 616
Db 541 tgagtgtcccggtgctgcgctgtcaaaaatcaccttagcgttgacggccaata 600
QY 617 acgcaaaaatgcgcgagagcttgcgcgagcgcgagaaatcccaacagtgtatatgtgaa 676
Db 601 acgcaaaaatgcgcgagagcttgcgcgagcgcgagaaatcccaacagtgtatatgtgaa 660
QY 677 atgctcaggcgaagggaatttccgagcgttttccggtgttagtcccccgaacatgagcc 736
Db 661 atgctcaggcgaagggaatttccgagcgttttccggtgttagtcccccgaacatgagcc 720
QY 737 ggtctgtaacccgcagtggtgtcagcgcgcagacccttgccttcaagttcgtctgcaaaa 796
Db 721 ggtctgtaacccgcagtggtgtcagcgcgcagacccttgccttcaagttcgtctgcaaaa 780
QY 797 actcgtgtatcgggcgaaaagaaacttcccttagtcttctgctgggaaagcatcgggcg 856
Db 781 actcgtgtatcgggcgaaaagaaacttcccttagtcttctgctgggaaagcatcgggcg 840
QY 857 atatcgtggacagcatgttatcatgttataaatatgtacgtgccccagcgggatcgca 916
Db 841 atatcgtggacagcatgttatcatgttataaatatgtacgtgccccagcgggatcgca 900
QY 917 tccaaagcaacccagcgtcaaatagcaagaagcgaagtcctgt jccggaagccgcggaag 976
Db 901 tccaaagcaacccagcgtcaaatagcaagaagcgaagtcctgt jccggaagccgcggaag 960
QY 977 aagatgagccgtccaaaggtgcgtgcgtgattgctataaagacgggagacacggagagca 1036
Db 961 aagatgagccgtccaaaggtgcgtgcgtgattgctataaagacgggagacacggagagca 1020
QY 1037 atgatagccgagactgcgacgactccgcgcgagagtggaacgtgtcgcggacacccgcatg 1096
Db 1021 atgatagccgagactgcgacgactccgcgcgagagtggaacgtgtcgcggacacccgcatg 1080
QY 1097 gogattaccgtctggttattacgtgccccaaataaggaatggctgtcgagag atcgagg 1156
Db 1081 gogattaccgtctggttattacgtgccccaaataaggaatggctgtcg agagcctcgagg 1140
QY 1157 gcatgattaaaggaggcggcggtgaagtctgcgcaatcccaaccaaagaagaatctacgtc 1216
Db 1141 gcatgattaaaggaggcggcggtgaagtctgcgcaatcccaaccaaagaagaatctacgtc 1200
QY 1217 gccatgccaaacaaattgctgagccttaaga 1246
Db 1201 gccatgccaaacaaattgctgagccttaaga 1230

RESULT 10
US-60-167-217-22996
; Sequence 22996, Application US/60167217
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000152
; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22996
; LENGTH: 5453
; TYPE: DNA
; ORGANISM: Drosophila
US-60-167-217-22996

Query Match 67.8%; Score 1067; DB 49; Length 5453;
Best Local Similarity 87.4%; Pred. No. 5.1e-297;
Matches 1282; Conservative 0; Mismatches 0; Indels 185; Gaps 3;

QY 292 cagcaatccgtgctgcgcgaaaatgatgtgcaggacattcagatccagcgcgaacgcgtg 351
Db 3362 cagcaatccgtgctgcgcgaaaatgatgtgcaggacattcagatccagcgcgaacgcgtg 3421
QY 352 cccaagctagagaatcaacaacatcgtgtgttattgttctcagcatgttctggatgagccg 411
Db 3422 cccaagctagagaatcaacaacatcgtgtgttattgttctcagcatgttctggatgagccg 3481
QY 412 cccaagctcttttggatgtactcgtatccgtgcgaagctctacatccggtatgaacaag 471
Db 3482 cccaagctcttttggatgtactcgtatccgtgcgaagctctacatccggtatgaacaag 3541
QY 472 gccttcaacgtggacgtttcagttcaagttaaaatgcccatcccaaccttaatttgcgt 531
Db 3542 gccttcaacgtggacgtttcagttcaagttaaaatgcccatcccaaccttaatttgcgt 3601
QY 532 gtgttctcttgccttctccaatgatgtgagtgctcccggtgcgtgcgttcaaaaatccctt 591
Db 3602 gtgttctcttgccttctccaatgatgtgagtgctcccggtgcgtgcgttcaaaaatccctt 3661
QY 592 agcgttgagcctt-----tgacggcccaataacgcgaataatgcgcgagagcttgcgcgag 604
Db 3662 agcgttgagccttgaagtgaagataacaatacacagatcgaaacaggattatttaactatca 3721
QY 605 -----tgacggcccaataacgcgaataatgcgcgagagcttgcgcgag 647
Db 3722 ttgtacaaaacctttagtgacggcccaataacgcgaataatgcgcgagagcttgcgcgag 3781
QY 648 cgagaatcccaacagtgatatattgtggaatgctcagggcaagggaatttccgagcgttt 707
Db 3782 cgagaatcccaacagtgatatattgtggaatgctcagggcaagggaatttccgagcgttt 3841
QY 708 ttccgttctgtagtcctccctgaacatgagccggtctgttaacccgcagtggtgcacgcgcca 767
Db 3842 ttccgttctgtagtcctccctgaacatgagccggtctgttaacccgcagtggtgcacgcgcca 3901
QY 768 gacctggccttcaagtctgtccaaaactcgtgtatcggggcgaagaacttccctt 827
Db 3902 gacctggccttcaagtctgtccaaaactcgtgtatcggggcgaagaagaacttccctt 3961
QY 828 agtcttctgcctggagaaaagcat----- 850
Db 3962 agtcttctgcctggagaaaagcatggttaagtgacagcaaaaactctagatggctagaacaa 4021
QY 851 -----gcgcgatatcgtgggacagcatgtttatcatgtt 885
Db 4022 agcttaacgtgttttcttcttcttgcagcggcgatatcgtgtggacagcatgtttatcatgtt 4081
QY 886 aaaatatgtacgtgccccaaagcgggatcgcatccaaagacgaacgccagctcaatagaag 945

```
|||||
Db 4082 aaatatgtacgtgccccaaagggtgacgcatccaaagaaagacccagctcaatagcaag 4141
QY 946 aagcgcaagtccgtgcccgaagccgcgaagaagatgagccgtccaaagtgctgctg 1005
Db 4142 aagcgcaagtccgtgcccgaagccgcgaagaagatgagccgtccaaagtgctgctg 4201
QY 1006 attgctataaaagacagcgagacacagcgagagcaaatgatagccgagactgcgacgactccg 1065
Db 4202 attgctataaaagacagcgagacacagcgagagcaaatgatagccgagactgcgacgactccg 4261
QY 1066 gcaagtggaacgtgtgcgcgacacccggagcgattaccgctggcctggaattacg 1125
Db 4262 gcaagtggaacgtgtgcgcgacacccggagcgattaccgctggcctggaattacg 4321
QY 1126 aataaggaatggctgctgcagagcagcagcagcagcagcagcagcagcagcagcagcagc 1185
Db 4322 aataaggaatggctgctgcagagcagcagcagcagcagcagcagcagcagcagcagcagc 4381
QY 1186 ctgcgcaatcccaacaaagagaaatctacgtccgcatgccaacaaatctgagccttaag 1245
Db 4382 ctgcgcaatcccaacaaagagaaatctacgtccgcatgccaacaaatctgagccttaag 4441
QY 1246 a----- 1246
Db 4442 agtaagcagtgaaatcgaggagacaaagagattaaagctttactaccgaacttcttcag 4501
QY 1247 aacgtgcctacgagctgccatgacttctgactgctgctgacaaatctcccaggtatcagata 1306
Db 4502 aacgtgcctacgagctgccatgacttctgactgctgctgacaaatctcccaggtatcagata 4561
QY 1307 cctttgaaatgtgtgcatctgtggtggtatatacatagctattagttatcttaagttgt 1366
Db 4562 cctttgaaatgtgtgcatctgtggtggtatatacatagctattagttatcttaagttgt 4621
QY 1367 attagtcctgtgtgtaaggcgtttaacggtgatatattcccttttggcagttgctgagtg 1426
Db 4622 attagtcctgtgtgtaaggcgtttaacggtgatatattcccttttggcagttgctgagtg 4681
QY 1427 cgaagaaacacatttttatattttgatagtagtactgttttaactgcagttctatgtg 1486
Db 4682 cgaagaaacacatttttatattttgatagtagtactgttttaactgcagttctatgtg 4741
QY 1487 actacgtacttttgtgtaccacacacacacacacacacacacacacacacacacacacacac 1546
Db 4742 actacgtacttttgtgtaccacacacacacacacacacacacacacacacacacacacacac 4801
QY 1547 ttattaaagagttgtcatattttgcaa 1573
Db 4802 ttattaaagagttgtcatattttgcaa 4828

RESULT 11
US-60-171-625-448
; Sequence 448, Application US/60171625
; GENERAL INFORMATION:
; APPLICANT: Skupski, Marian
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS THAT SHOW
; TITLE OF INVENTION: HIGH HOMOLOGY TO KNOWN HUMAN DISEASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000179
; CURRENT APPLICATION NUMBER: US/60/171,625
; CURRENT FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 5453
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-171-625-448

Query Match 67.8%; Score 1067; DB 50; Length 5453;
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Best Local Similarity 87.4%; Pred. No. 5.1e-297;
Matches 1282; Conservative 0; Mismatches 0; Indels 185; Gaps 3;

QY 292 cagcaatccgtgctgcgcgaatgatgctgcaggacattcagatccaggcgcaacacgctg 351
Db 3362 cagcaatccgtgctgcgcgaatgatgctgcaggacattcagatccaggcgcaacacgctg 3421
QY 352 ccaagctagagaatcacacacatcggtgttattgtcttcagcatggttctggatgagcgg 411
Db 3422 ccaagctagagaatcacacacatcggtgttattgtcttcagcatggttctggatgagcgg 3481
QY 412 ccaagctctcttggatgtactcgtattccgctgaacaagctctacatcccgatgaacaag 471
Db 3482 ccaagctctcttggatgtactcgtattccgctgaacaagctctacatcccgatgaacaag 3541
QY 472 gcctcaacgtgcgacgttcaagtccaagttaaaatgccatcccaacacacacacacacac 531
Db 3542 gcctcaacgtgcgacgttcaagtccaagttaaaatgccatcccaacacacacacacacac 3601
QY 532 gtgttccttcttccatcgaatgtgagtgctcccggtgcgcgtgcgcgtgcgcacacacac 591
Db 3602 gtgttccttcttccatcgaatgtgagtgctcccggtgcgcgtgcgcgtgcgcacacacac 3661
QY 592 agcgttgagcctt----- 604
Db 3662 agcgttgagccttgaagtgaagataacaatacacagatcgaaacaggattatttaactatca 3721
QY 605 -----tgacggccaataaaccaaaaatgcgcgagagcttgcgcgcag 647
Db 3722 ttgtacaaaacccctttagtgacggccaataaaccaaaaatgcgcgagagcttgcgcgcag 3781
QY 648 cgagaatcccaacacagtgatatattgtgaaatgctcaggggcaagggaaatttccgagcgttt 707
Db 3782 cgagaatcccaacacagtgatatattgtgaaatgctcaggggcaagggaaatttccgagcgttt 3841
QY 708 ttccgttgtagtcccccgaacatgagccgtgtgttaaccccgagtggtgcacgcgcga 767
Db 3842 ttccgttgtagtcccccgaacatgagccgtgtgttaaccccgagtggtgcacgcgcga 3901
QY 768 gaccctgaccttcaagttcgtctgcacaaactcgtgtatcggcgcaaaagaaactcctt 827
Db 3902 gaccctgaccttcaagttcgtctgcacaaactcgtgtatcggcgcaaaagaaactcctt 3961
QY 828 agtcttgcctggagaaagcat----- 850
Db 3962 agtcttgcctggagaaagcatggttaagtgacagcaaaactctagatggctagaacaa 4021
QY 851 -----gcgcgcatatcgtgggacagcatgtttatcatgtt 885
Db 4022 agcttaacgtgttttcttcttgcagcgcgcatatcgtgggacagcatgtttatcatgtt 4081
QY 886 aaaaatgtacgtgccccaaagcggtatcgcatcaagacgaacccagctcaatagcaag 945
Db 4082 aaaaatgtacgtgccccaaagcggtatcgcatcaagacgaacccagctcaatagcaag 4141
QY 946 aagcgcaagtccgtgcccgaagccgcgaagaagatgagccgtccaaaggtgcgtcggtgc 1005
Db 4142 aagcgcaagtccgtgcccgaagccgcgaagaagatgagccgtccaaaggtgcgtcggtgc 4201
QY 1006 attgctataaaagacgagggacacgagagcaatgatagccgagactgcgacgactccg 1065
Db 4202 attgctataaaagacgagggacacgagagcaatgatagccgagactgcgacgactccg 4261
QY 1066 gcagagtggaaacgtgtgcgcgacacccggatggcgattaccgtcttggtattacgtgccc 1125
Db 4262 gcagagtggaaacgtgtgcgcgacacccggatggcgattaccgtcttggtattacgtgccc 4321
QY 1126 aataaggaatggctgctgcagagcagcagcagcagcagcagcagcagcagcagcagcagc 1185
Db 4322 aataaggaatggctgctgcagagcagcagcagcagcagcagcagcagcagcagcagcagc 4381
QY 1186 ctgcgcaatcccaacaaagagaaatctacgtccgcatgccaacaaatctgagccttaag 1245
|||||
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Db 4382 ctgcgcaatcccaacgaagagaatctctacgtcgccatgcccaacaaattgctgagccttaag 4441
QY 1246 a-----1246
Db 4442 agtaagcagtgaaatcgaggacaaagagattagccttaacttaaccgaacttcccttcaag 4501
QY 1247 aacgtgctacagagtgccatgacttctgtatctggtcgacaaatctccaggtatcagata 1306
Db 4502 aacgtgctacagagtgccatgacttctgtatctggtcgacaaatctccaggtatcagata 4561
QY 1307 cctttgaaatgtgtgcatctgtgggtatatactacatagcta: agtatcttaagtgtg 1366
Db 4562 cctttgaaatgtgtgcatctgtgggtatatactacatagcta: agtatcttaagtgtg 4621
QY 1367 attagtcctgttctgtaaggcgttttaacggtgatacttccctt: tggcatgttgcagatggc 1426
Db 4622 attagtcctgttctgtaaggcgttttaacggtgatacttccctt: tggcatgttgcagatggc 4681
QY 1427 cgaaaaaagaaacatttttatattttttgtagtagtatactgtttgttaactgcagttctatgtg 1486
Db 4682 cgaaaaaagaaacatttttatattttttgtagtagtatactgtttgttaactgcagttctatgtg 4741
QY 1487 actacgtaacttttctaccacaaacatactctgtacaaaagcgaaggaatgaat 1546
Db 4742 actacgtaacttttctaccacaaacatactctgtacaaaagcgaaggaatgaat 4801
QY 1547 ttattaaagagtggtcatattttgcaa 1573
Db 4802 ttattaaagagtggtcatattttgcaa 4828

RESULT 12
US-60-173-464-18651
; Sequence 18651, Application US/60173464
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W.D.
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000173
; CURRENT APPLICATION NUMBER: US/60/173,464
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 30269
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18651
; LENGTH: 5453
; TYPE: DNA
; ORGANISM: Drosophila
US-60-173-464-18651

Query Match 67.8%; Score 1067; DB 50; Length 5453;
Best Local Similarity 87.4%; Pred. No. 5.1e-297;
Matches 1282; Conservative 0; Mismatches 0; Indels 185; Gaps 3;

QY 292 cagcaatccgtgctgcgcaaatgatgtcgaggaacattcagatccagcgcaacacgctg 351
Db 3362 cagcaatccgtgctgcgcaaatgatgtcgaggaacattcagatccagcgcaacacgctg 3421
QY 352 cccaagctagagaatcacacatcggtgttattgtttcagca:ggttctggatgagccg 411
Db 3422 cccaagctagagaatcacacatcggtgttattgtttcagca:ggttctggatgagccg 3481
QY 412 cccaagctcttttgatgtactcgattccgcaagaaagctctacatccggtatgaacaaag 471
Db 3482 cccaagctcttttgatgtactcgattccgcaagaaagctctacatccggtatgaacaaag 3541
QY 472 geettcaacgtggaacttcagttcgaagttcaaatgcccacatcccaacttaatttgcgt 531
Db 3542 geettcaacgtggaacttcagttcgaagttcaaatgcccacatcccaacttaatttgcgt 3601
QY 532 gtgttcctttgtctctccaatgatgtgagtgctcccggtccggtgcgaataacacett 591

Db 3602 gtgttcctttgtcttcccaatgatgtgagtgctcccggtggtccgctgtcaaaatcacctt 3661
QY 592 agcgttgagcctt-----604
Db 3662 agcgttgagccttgaagtgaagataaacaatacacagatcgaaacaggattattttaactalca 3721
QY 605 -----tgacggccaataaacgcaaaaaatcgcgagagcttgcgcgcag 647
Db 3722 ttgtcaaaaaccttttagtgacggccaataaacgcaaaaaatcgcgagagcttgcgcgcag 3781
QY 648 cgagaatcccaacagtggtatattgtggaatgctcaggggcaagggaatttccgagcgttt 707
Db 3782 cgagaatcccaacagtggtatattgtggaatgctcaggggcaagggaatttccgagcgttt 3841
QY 708 ttccgttgtagtccccctgaacatgagccggtctgttaaccccgagtggtgcacgcgcga 767
Db 3842 ttccgttgtagtccccctgaacatgagccggtctgttaaccccgagtggtgcacgcgcga 3901
QY 768 gacctggccttcaagtctgtctgcacaaactgtgtatcgggcgaaaaaagaaacttccctt 827
Db 3902 gacctggccttcaagtctgtctgcacaaactgtgtatcgggcgaaaaaagaaacttccctt 3961
QY 828 agtcttctgctggagaaagcat-----850
Db 3962 agtcttctgctggagaaagcatggttaaggtgacagcaaaaacttagatggctagaacaa 4021
QY 851 -----ggggcgatatctgtgggacagcatgtttatacatgtt 885
Db 4022 agcttaacgtgttttcttcttgcagggcgatctgtgggacagcatgtttatacatgtt 4081
QY 886 aaaatatgtactgtgccccaaagcgggacatccaaagacgaacgcagctcaatagcaag 945
Db 4082 aaaatatgtactgtgccccaaagcgggacatccaaagacgaacgcagctcaatagcaag 4141
QY 946 aagcgcgaagtccgtgcccgaagccgcgaagaagatgagccgtccaaaggtgcgtcggtgc 1005
Db 4142 aagcgcgaagtccgtgcccgaagccgcgaagaagatgagccgtccaaaggtgcgtcggtgc 4201
QY 1006 attgctataaagacggagagacacggagagcaaatgatagccgagactgcgacgactccgcc 1065
Db 4202 attgctataaagacggagagacacggagagcaaatgatagccgagactgcgacgactccgcc 4261
QY 1066 gcagagtggaacgtgtgcgggacacccggatggcgattaccgtctggtattacgtgcccc 1125
Db 4262 gcagagtggaacgtgtgcgggacacccggatggcgattaccgtctggtattacgtgcccc 4321
QY 1126 aataaggaatggctgtgcagagcatcgagggcatgattaaaggagggcggtggaagtc 1185
Db 4322 aataaggaatggctgtgcagagcatcgagggcatgattaaaggagggcggtggaagtc 4381
QY 1186 ctgcgcaatcccaacccaagaagaatctactgtggtgtatactacatagatttagttttgt 1245
Db 4382 ctgcgcaatcccaacccaagaagaatctactgtggtgtatactacatagatttagttttgt 4441
QY 1246 a-----1246
Db 4442 agtaagcagtgaaatcgaggacaaagagattaaagctttacttaccgaacttcccttcaag 4501
QY 1247 aacgtgctacagagtgccatgacttctgtatctggtcgacaaatctccaggtatcagata 1306
Db 4502 aacgtgctacagagtgccatgacttctgtatctggtcgacaaatctccaggtatcagata 4561
QY 1307 cctttgaaatgtgtgcatctgtgggtatactacatagatttagttttgt 1366
Db 4562 cctttgaaatgtgtgcatctgtgggtatactacatagatttagttttgt 4621
QY 1367 attagtcctgttgcgtaaggcgttttaacggtgatacttcccttttggcatgttgcagatggc 1426
Db 4622 attagtcctgttgcgtaaggcgttttaacggtgatacttcccttttggcatgttgcagatggc 4681
QY 1427 cgaaaaaagaaacatttttatattttttgtagtagtatactgtttgtaactgaagttctatgtg 1486
Db 4682 cgaaaaaagaaacatttttatattttttgtagtagtatactgtttgtaactgaagttctatgtg 4741

; NUMBER OF SEQ ID NOS: 30973
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17940
; LENGTH: 5454
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-681-17940

Query Match 67.8%; Score 1067; DB 52; Length 5454;
Best Local Similarity 87.4%; Pred. No. 5.1e-297;
Matches 1282; Conservative 0; Mismatches 0; Indels 185; Gaps 3;

QY 292 cagcaatccgtgctgcggaatgatgctgcaggacattcagatccagcggaacacgctg 351
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Db 2092 CAGCAATCCGTGCTGCGGAAATGATGCTGCAGGACATTCAGATCCAGGCGAACACGCTG 2033
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QY 352 cccaagctagagaatacacaacatcggtggttattgcttcagcatggttctggatgagcgg 411
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Db 2032 CCCAAGCTAGAGAAATCAACAACATCGGTGTTATTGCTTCAGCATGGTCTCTGGATGAGCCG 1973
|||||
QY 412 cccaagctcttttgatgactcgtattccgctgaacaagctctacatccggatgaacaag 471
|||||
Db 1972 CCCAAGCTCTTTGGATGTACTCGATTCCGCTGAACAAGCTCTACATCCGGATGAACAAG 1913
|||||
QY 472 gccttcaacgtggacgttcagttcaagtctaaatgctccatccacacacttaattgcgt 531
|||||
Db 1912 GCCTTCAACGTGGACGTTCAAGTCTAAGTCTAAATGCCCATCCAACACTTAATTGCGT 1853
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QY 532 gtgttcctttgcttctccaatgatgtgagtgctcccggtggtccgtgctcaaaatcaacctt 591
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Db 1852 GTGTTCCTTTGCTTCTCCAATGATGTGAGTGCTCCCGGTGCTCCGCTGTCAAAATCACCTT 1793
|||||
QY 592 agcgttgagcctt----- 604
|||||
Db 1792 AGCGTTGAGCCTTTGTAAGTGAAGATAACAATAACAGATCGAACAGGATTATTAACTATCA 1733
|||||
QY 605 -----tgacggccaataaacycaaaaatgcgcgagagcttgctgcgcag 647
|||||
Db 1732 TTGTACAAACCTTTAGTGACGGCCAAATACGCAAAATGCGCGAGAGCTTGCTGCGCAG 1673
|||||
QY 648 cgagaatcccaacagtgatatgttggaatgctcagggcaagggaatttccgagcgttt 707
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Db 1672 CGAGAATCCCAACAGTGATATTTGTGGAATGCTCAGGGCAAGGGAATTTCCGAGCGTTT 1613
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QY 708 ttccgttgtagtccccctgaacatgagccggtctgtaccccgagtggttcacgcgcca 767
|||||
Db 1612 TTCCGTTGTAGTCCCCCTGAACATGAGCCGCTGTGTAAACCCCGAGTGGCTCACCGGCCA 1553
|||||
QY 768 gacctggcctcaagtctgctgcgaactcgtgtatcggtgcggaagaaacttcctt 827
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Db 1552 GACCTGGCCTTCAAGTTCCTCTGCCAAACTCGTGTATCGGGCGGAAAGAAACTTCCTT 1493
|||||
QY 828 agtcttctgctggagaaagcat----- 850
|||||
Db 1492 AGTCTTCTGCTGGAGAAAGCATGGTAAGGTGACAGCAAAACTCTAGATGGCTAGAACAA 1433
|||||
QY 851 -----gcgcgatatcgtgggacagcatgttatacatgtt 885
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Db 1432 ACCTTAACGTGTTTTCTTTCTTGACGGCGCATATCGTGGACAGCATGTTTATACATGTT 1373
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QY 886 aaaaatatgactgccccagcgggatcgcatccaaagcgaacgcagctcaatagaag 945
|||||
Db 1372 AAATATGTACGTGCCCCAAGCGGGATCGCATCCAAGACCAACGCCAGCTCAATAGCAAG 1313
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QY 946 aagcgcaagtccgtgcccgaagccgcgaagaagatgagccgtccaaagtgctcgatgc 1005
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Db 1312 AAGCGCAAGTCCGTGCGGAAAGCCCGCAAGAAGATGAGCCGTCCAAGGTGCGTCCGTGC 1253
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QY 1006 attgctataaagacgagagacacgagagcaatgatagcagactgagcagactccgccc 1065
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QY 1066 gcagagtggaacgctgctgcggaacacggatgctgacattaccgtctggctattacgtgcccc 1125
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Db 1192 GCAGAGTGGAAACGTGTCGGGACACCGGATGGGATTACCGTCTGGCTATTACGTGCCCC 1133
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QY 1126 aataaggaatggctgctgcagagcagcagggcagcagcagcagcagcagcagcagcagc 1185
|||||
Db 1132 AATAAGGAATGGCTGCTGCAGAGCATCGAGGGCATGATTAAGGAGCGCGGCTGAAGTC 1073
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QY 1186 ctgcgcaatcccaacaaagagaatctacgtgcgcacatgccaacaaattgctgagccttaag 1245
|||||
Db 1072 CTGCGCAATCCCAACCAAGAGAATCTACGTGCGCATGCCAACAATGCTGAGCCTTAAG 1013
|||||
QY 1246 a----- 1246
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Db 1012 AGTAAGCAGTGAATCGGAGGACAAAGAGATTAAAGCTTTACTTACCGAACTTTCCCTTCAG 953
|||||
QY 1247 aacgtgcctacagagctgcccagctctctgatctgtgcagacaatctcccaggtatcagata 1306
|||||
Db 952 AACGTGCTACGAGCTGCCATGACTTCTGATCTGGTCGACAAATCTCCCAGGTATCAGATA 893
|||||
QY 1307 ccttgaaatgtgtgcatctgtggtggtatatactacatagctattagttatcttaagtgtg 1366
|||||
Db 892 CCTTTGAATGTGTGCTATCTGTGGGTATATACTATAGCTATTAGTATCTTAAGTTGT 833
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QY 1367 attagtcctgttcgtaaggcgtttaacggtgatattcccccttttggcatgttcgatggc 1426
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Db 832 ATTAGTCTCTGTTGTAAGCGGTTTAAAGGTTGATATCCCTTTTGGCATGTTTCGATGGC 773
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QY 1427 cgaaaagaaaacatttttatatttttagtagtagtatactgttgaactgcagttctatgtg 1486
|||||
Db 772 CGAAAAGAAAACATTTTATATTTTGTAGTAGTATACTGTGTTAACTGCAGTCTATGTG 713
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QY 1487 actacgtaaacttttctaccacaacacatactctgtacaaaaaaagccaaaagtgaat 1546
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Db 712 ACTACGTACTTTTGTCTACCAACACACATCTCTGTACAAAAAGCCAAAAGTGAAT 653
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QY 1547 ttattaaagagtgctcatatttttgcga 1573
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Db 652 TTATTAAAGAGTGTTCATATTTTGCAG 626
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RESULT 15
US-09-268-969-7
; Sequence 7, Application US/09268969
; GENERAL INFORMATION:
; APPLICANT: Buchman, Andrew R.
; APPLICANT: Platt, Darren M.
; APPLICANT: Ollmann, Michael M.
; APPLICANT: Young, Lynn M.
; APPLICANT: Demsky, Madelyn R.
; APPLICANT: Keegan, Kevin P.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENES AND USES THEREOF
; FILE REFERENCE: 7326-084
; CURRENT APPLICATION NUMBER: US/09/268,969
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 8805
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-268-969-7

Query Match 67.8%; Score 1067; DB 16; Length 8805;
Best Local Similarity 87.4%; Pred. No. 6.4e-297;
Matches 1282; Conservative 0; Mismatches 0; Indels 185; Gaps 3;
QY 292 cagcaatccgtgctgcggaatgatgctgcaggacattcagatccagcggaacacgctg 351
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Db 3599 cagcaatccgtgctgcggaatgatgctgcaggacattcagatccagcggaacacgctg 3658
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QY 352 cccaagctagagaatcacacaatcggtggttattgcttcagcatggttctggatgagcg 411
|||||
Db 3659 cccaagctagagaatcacacaatcggtggttattgcttcagcatggttctggatgagcg 3718
QY 412 cccaagtctctttggatgtactcgattccgctgaacaaagctctacatccggatgaacaa 471
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Db 3719 cccaagtctctttggatgtactcgattccgctgaacaaagctctacatccggatgaacaa 3778
QY 472 gccttcaacgtgacgttccagtccaagtctaaaaatgccatcccaaccacttaatttgct 531
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Db 3779 gccttcaacgtgacgttccagtccaagtctaaaaatgccatcccaaccacttaatttgct 3838
QY 532 gtgttcccttgccttccaatgatgtgagtgctcccggtggtccgctgtcaaaatcacctt 591
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Db 3839 gtgttcccttgccttccaatgatgtgagtgctcccggtggtccgctgtcaaaatcacctt 3898
QY 592 agcgttgagcctt----- 604
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Db 3899 agcgttgagccttctaagtgaagataacaataacagatcgaaacaggattatttaactatca 3958
QY 605 -----tgacggccaataaacgcaaaaaatgcgcgagagcttgctgcgcag 647
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Db 3959 ttgtacaaaaccttttagtgacggccaataaacgcaaaaaatgcgcgagagcttgctgcgcag 4018
QY 648 cgagaatcccaacacagtgatatattgtggaaaatgctcaggggcaagggaatttccgagcgctt 707
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Db 4019 cgagaatcccaacacagtgatatattgtggaaaatgctcaggggcaagggaatttccgagcgctt 4078
QY 708 ttccgtttagtccctgaacatgagccggtctgtaaccgcagtggtggctcacgcgcga 767
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Db 4079 ttccgtttagtccctgaacatgagccggtctgtaaccgcagtggtggctcacgcgcga 4138
QY 768 gaccttgcccttcaagttcgtctgcacaaactcgtgtatcggggcaaaaagaaacttcctt 827
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Db 4139 gaccttgcccttcaagttcgtctgcacaaactcgtgtatcggggcaaaaagaaacttcctt 4198
QY 828 agtcttctgcctggagaaaagcat----- 850
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Db 4199 agtcttctgcctggagaaaagcatgtaaggtagacagcaaaactctagatggctagaacaa 4258
QY 851 -----gcggcgatatcgttgggacagcatgtttatatacatgtt 885
|||||
Db 4259 agcttaacgtgttttcttcttgacgcgcgatatacgttgggacagcatgtttatatacatgtt 4318
QY 886 aaaatatgtacgtgccccaaagcgggatacgatccaaagacgaacgccagctcaatagcaag 945
|||||
Db 4319 aaaatatgtacgtgccccaaagcgggatacgatccaaagacgaacgccagctcaatagcaag 4378
QY 946 aagcgcaagtcctgccccgaagccccgcgaagaagatgagccgtccaaggtgcgtggtgc 1005
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Db 4379 aagcgcaagtcctgccccgaagccccgcgaagaagatgagccgtccaaggtgcgtggtgc 4438
QY 1006 attgctataaagacgggagacacggaggaatgatagccgagactgcgacgactccgcc 1065
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Db 4439 attgctataaagacgggagacacgggaggaatgatagccgagactgcgacgactccgcc 4498
QY 1066 gcagagtggaaacgtgtcgcgggacacccggatggcgattaccgtctggctattacgtgcccc 1125
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QY 1126 aataaaggaatggctgctgcagagacatcgaggggcatgattaaggcgcggtgaagtc 1185
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Db 4559 aataaaggaatggctgctgcagagacatcgaggggcatgattaaggcgcggtgaagtc 4618
QY 1186 ctgcgcaatcccaaccacgaagaatctacgtcgccatgcgaacaaatgtgagccttaag 1245
|||||
Db 4619 ctgcgcaatcccaaccacgaagaatctacgtcgccatgcgaacaaatgtgagccttaag 4678
QY 1246 a----- 1246
|
Db 4679 agtaagcagtgaaatcgaggacaaagagattaagctttacttaccgaacttccctttcag 4738
QY 1247 aacgtgcctacgagctgccatgacttctgtatctggtgcgacaaatctcccagggtatcagata 1306

Db 4739 aacgtgcctacgagctgccatgacttctgatctggtcgacaatctcccagggtatcagata 4798
QY 1307 cctttgaaaatgtgttgcatctctggtgggtatactacatagctatttagtatctttaagtttgt 1366
|||||
Db 4799 cctttgaaaatgtgttgcatctctggtgggtatactacatagctatttagtatctttaagtttgt 4858
QY 1367 attagtccttgttgctaaaggcggtttaacgggtgatattcccttttggcatgttccgatggc 1426
|||||
Db 4859 attagtccttgttgctaaaggcggtttaacgggtgatattcccttttggcatgttccgatggc 4918
QY 1427 cgaaaaagaaaaacatttttatatttttgatagtagtctgtttaaactgcagttcttatgtg 1486
|||||
Db 4919 cgaaaaagaaaaacatttttatatttttgatagtagtctgtttaaactgcagttcttatgtg 4978
QY 1487 actacgtaaacttttgcctaccacacacaaacatactctgtacacaaaaagccaaaaagtgaat 1546
|||||
Db 4979 actacgtaaacttttgcctaccacacacaaacatactctgtacacaaaaagccaaaaagtgaat 5038
QY 1547 ttattaaagagttgtcattatattttgcaa 1573
|||||
Db 5039 ttattaaagagttgtcattatattttgcaa 5065

Search completed: November 16, 2001, 15:47:04
Job time: 6151 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2001, 14:25:13 ; Search time 86.49 Seconds
(without alignments)
4456.618 Million cell updates/sec

Title: US-09-524-101-1
Perfect score: 1573
Sequence: 1 aaaaatccaaatagtcggtgg.....agagttgtcatattttgcaa 1573

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 128180 seqs, 122521576 residues

Total number of hits satisfying chosen parameters: 256360

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	37.4	2.4	8093	5 US-09-897-516-203	Sequence 203, App
C 2	37.4	2.4	8093	5 US-09-897-516-204	Sequence 204, App
C 3	37.4	2.4	8093	5 US-09-897-516-1930	Sequence 1930, Ap
C 4	37.4	2.4	8093	5 US-09-897-516-1931	Sequence 1931, Ap
C 5	37.4	2.4	8093	5 US-09-897-516-1932	Sequence 1932, Ap
C 6	37.4	2.4	8093	5 US-09-897-516-1933	Sequence 1933, Ap
C 7	37.4	2.4	8093	5 US-09-897-516-1934	Sequence 1934, Ap
C 8	37	2.4	1811	6 US-60-325-448-3646	Sequence 3646, Ap
C 9	34.2	2.2	1320	5 US-09-815-242-4152	Sequence 4152, Ap
C 10	33	2.1	261	5 US-09-388-906A-15677	Sequence 15677, A
C 11	33	2.1	327	5 US-09-680-959-564	Sequence 564, App
C 12	32.6	2.1	2664	5 US-09-815-242-9081	Sequence 9081, Ap
C 13	32.4	2.1	4370	5 US-09-976-594-885	Sequence 885, App
C 14	32.4	2.1	14800	5 US-09-954-456-1601	Sequence 1601, Ap
C 15	32.2	2.0	425	5 US-09-834-975-451	Sequence 451, App
C 16	32	2.0	466	5 US-09-922-340-8358	Sequence 8358, Ap
C 17	32	2.0	2000	6 US-60-325-448-2079	Sequence 2079, Ap
C 18	31.6	2.0	363	5 US-09-388-906A-4998	Sequence 4998, Ap
C 19	31.6	2.0	429	5 US-09-922-340-10883	Sequence 10883, A
C 20	31.6	2.0	627	6 US-60-325-448-388	Sequence 388, App
C 21	31.6	2.0	678	5 US-09-815-242-7612	Sequence 7612, Ap
C 22	31.6	2.0	402850	5 US-09-844-653-5	Sequence 5, Appli
C 23	31.2	2.0	639	6 US-60-325-448-4487	Sequence 4487, Ap
C 24	31.2	2.0	1008	5 US-09-976-594-1049	Sequence 1049, Ap
C 25	31.2	2.0	25871	5 US-09-798-743A-5	Sequence 5, Appli
C 26	31.2	2.0	1503841	5 US-09-795-668-1	Sequence 1, Appli
C 27	31	2.0	660	5 US-09-370-861A-32	Sequence 32, Appl

C 28	31	2.0	1511	5 US-09-370-861A-8	Sequence 8, Appli
C 29	30.8	2.0	460	5 US-09-388-906A-21420	Sequence 21420, A
C 30	30.8	2.0	777	5 US-09-815-242-7859	Sequence 7859, Ap
C 31	30.6	1.9	675	5 US-09-815-242-4264	Sequence 4264, Ap
C 32	30.6	1.9	738	5 US-09-815-242-8498	Sequence 8498, Ap
C 33	30.6	1.9	1163	6 US-60-325-448-3429	Sequence 3429, Ap
C 34	30.6	1.9	1960	5 US-09-834-975-833	Sequence 833, App
C 35	30.4	1.9	352	5 US-09-969-373-344	Sequence 344, App
C 36	30.4	1.9	705	5 US-09-815-242-7320	Sequence 7320, Ap
C 37	30.2	1.9	264	5 US-09-388-906A-23549	Sequence 23549, A
C 38	30.2	1.9	7419	5 US-09-815-242-4009	Sequence 4009, Ap
C 39	30	1.9	396	5 US-09-388-906A-5376	Sequence 5376, Ap
C 40	30	1.9	535	5 US-09-388-906A-3612	Sequence 3612, Ap
C 41	30	1.9	957	5 US-09-886-055-80	Sequence 80, Appl
C 42	29.8	1.9	396	5 US-09-970-966-57	Sequence 57, Appl
C 43	29.8	1.9	403	5 US-09-388-906A-17909	Sequence 17909, A
C 44	29.8	1.9	799	5 US-09-976-594-887	Sequence 887, App
C 45	29.8	1.9	2000	6 US-60-325-448-2192	Sequence 2192, Ap

ALIGNMENTS

RESULT 1
US-09-897-516-203/c
; Sequence 203, Application US/09897516
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Huesing, Joseph E.
; APPLICANT: Krasomil-Osterfeld, Karina C.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Slater, Steven C.
; APPLICANT: Spiridonov, Sergei
; TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51847)B
; CURRENT APPLICATION NUMBER: US/09/897,516
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215, 161
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 8409
; SEQ ID NO 203
; LENGTH: 8093
; TYPE: DNA
; ORGANISM: Xenorhabdus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (705)..(1919)
US-09-897-516-203

Query Match	2.4%	Score 37.4;	DB 5;	Length 8093;
Best Local Similarity	53.0%	Pred. No. 2.1;		
Matches	80;	Conservative	0;	Mismatches 71;
				Indels 0;
				Gaps 0;
QY 1039	gatagccgagactgcgacgactccgcccgcagagtggaacgtgtcgcggacacccggatggc	1098		
Db 509	GATAACAATCCCTTCGTCGTCTTCGTACCAACGCGTTCACCGTCCCGGGCGACCGGAAAGC	450		
QY 1099	gattaccgtctggtattacgtgcccataaagaatggtgtcgcagagatcgagggc	1158		
Db 449	AAAGGACGACTGGGTAATATCGCCCGCTGCAAGGGAGCCAGCACCATCCCGGATGGT	390		
QY 1159	atgattaaggagcgcggtgctgaagtcctgc	1189		
Db 389	CTGATTATCGGGGCGCTGAATGCTGTATTGC	359		

RESULT 2
US-09-897-516-204/c
; Sequence 204, Application US/09897516
; GENERAL INFORMATION:

Query Match 2.4%; Score 37.4; DB 5; Length 8093;
Best Local Similarity 53.0%; Pred. No. 2.1;

RESULT 5
US-09-897-516-1932/c
; Sequence 1932, Application US/09897516
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Huesing, Joseph E.
; APPLICANT: Krasomal-Osterfeld, Karina C.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Slater, Steven C.
; APPLICANT: Spiridonov, Sergel

Db 449 AAAGGACGACTGGGTAATATCGCCCCCGTGTCAAGGAGCCAGACCAATCCCGGATGGT 390

Qy 1159 atgattaaggaggcgcggtgaagtctgc 1189
 ||||| | | | | | | | | | | | |

Db 389 CTGATTATCGGGGCGCTGAATGCTGTATTGC 359

RESULT 7

US-09-897-516-1934/C

; Sequence 1934, Application US/09897516

; GENERAL INFORMATION:

; APPLICANT: Corbin, David R.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Huesing, Joseph E.

; APPLICANT: Krasomil-Osterfeld, Karina C.

; APPLICANT: Malvar, Thomas M.

; APPLICANT: Slater, Steven C.

; APPLICANT: Spiridonov, Sergei

; TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof

; FILE REFERENCE: 38-21(51847)B

; CURRENT APPLICATION NUMBER: US/09/897,516

; CURRENT FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/215, 161

; PRIOR FILING DATE: 2000-06-30

; NUMBER OF SEQ ID NOS: 8409

; SEQ ID NO 1934

; LENGTH: 8093

; TYPE: DNA

; ORGANISM: Xenorhabdus sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (6435)..(7883)

US-09-897-516-1934

Query Match 2.4%; Score 37.4; DB 5; Length 8093;

Best Local Similarity 53.0%; Pred. No. 2.1;

Matches 80; Conservative 0; Mismatches 71; Indels 0; Gaps

Qy 1039 gatagccgagactgcgacgactccgcgcagagtggaaactgtcgcggacaccggtggc 1098
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Db 509 GATAACAATCCCTTCGTCGTCCTCGTACCAAGCGTTCACCGTCCCGGGCGACCCGGAAGC 450

Qy 1099 gattaccgctcgtggtattacgtgcccccaataaaggaatggctgtgcagagcatcgagggc 1158
 | | | | | | | | | | | | | | | | | | | | | |

Db 449 AAAGGACGACTGGGTAATATCGCCCCCGTGTCAAGGAGCCAGACCAATCCCGGATGGT 390

Qy 1159 atgattaaggaggcgcggtgaagtctgc 1189
 ||||| | | | | | | | | | | | |

Db 389 CTGATTATCGGGGCGCTGAATGCTGTATTGC 359

RESULT 8

US-60-325-448-3646

; Sequence 3646, Application US/60325448

; GENERAL INFORMATION:

; APPLICANT: Budworth, P.R.

; APPLICANT: Moughamer, T.G.

; TITLE OF INVENTION: Constitutive rice promoters

; FILE REFERENCE: 1360.026PRV

; CURRENT APPLICATION NUMBER: US/60/325,448

; CURRENT FILING DATE: 2001-09-26

; NUMBER OF SEQ ID NOS: 4708

; SEQ ID NO 3646

; LENGTH: 1811

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-60-325-448-3646

Query Match 2.4%; Score 37; DB 6; Length 1811;

Best Local Similarity 49.2%; Pred. No. 1.4;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2001, 15:47:13 ; Search time 241.3 Seconds
(without alignments)
443.009 Million cell updates/sec

Title: US-09-524-101-2
Perfect score: 2008
Sequence: 1 MYISQPMWSWKSTSEDDSDS.....NLRHANKLLSLKRAYELP 385

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
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7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
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9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
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15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2008	100.0	385	1	PCT-US00-06602-2	Sequence 2, Appli
2	2008	100.0	385	1	PCT-US00-06602A-2	Sequence 2, Appli
3	2008	100.0	385	16	US-09-268-969-2	Sequence 2, Appli
4	2008	100.0	385	19	US-09-524-101-2	Sequence 2, Appli
5	1973	98.3	381	24	US-60-167-217-22998	Sequence 22998, A
6	1973	98.3	381	24	US-60-171-625-450	Sequence 450, App
7	1973	98.3	381	24	US-60-173-464-18653	Sequence 18653, A
8	1973	98.3	381	24	US-60-191-637-22730	Sequence 22730, A
9	1973	98.3	381	24	US-60-191-681-17942	Sequence 17942, A

10	300.5	15.0	354	1	PCT-US00-06602-4	Sequence 4, Appli
11	300.5	15.0	354	1	PCT-US00-06602A-4	Sequence 4, Appli
12	300.5	15.0	354	19	US-09-524-101-4	Sequence 4, Appli
13	247.5	12.3	350	1	PCT-US00-06602-6	Sequence 6, Appli
14	247.5	12.3	350	1	PCT-US00-06602A-6	Sequence 6, Appli
15	247.5	12.3	350	19	US-09-524-101-6	Sequence 6, Appli
16	191	9.5	420	16	US-09-277-196-20	Sequence 20, Appli
17	191	9.5	499	1	PCT-US99-14057-2	Sequence 2, Appli
18	191	9.5	499	15	US-09-125-005-19	Sequence 19, Appli
19	191	9.5	499	15	US-09-174-493-26	Sequence 26, Appli
20	191	9.5	635	14	US-09-081-975-3	Sequence 3, Appli
21	191	9.5	636	1	PCT-US99-14057-1	Sequence 1, Appli
22	191	9.5	636	15	US-09-125-005-6	Sequence 6, Appli
23	191	9.5	636	21	US-09-732-384-10	Sequence 10, Appli
24	190	9.5	499	15	US-09-125-005-4	Sequence 4, Appli
25	190	9.5	637	15	US-09-125-005-2	Sequence 2, Appli
26	186	9.3	448	15	US-09-174-493-15	Sequence 15, Appli
27	186	9.3	448	19	US-09-542-615A-340	Sequence 340, App
28	186	9.3	448	20	US-09-606-421A-340	Sequence 340, App
29	186	9.3	448	20	US-09-630-940A-340	Sequence 340, App
30	186	9.3	448	20	US-09-630-940B-340	Sequence 340, App
31	186	9.3	448	20	US-09-643-597-340	Sequence 340, App
32	186	9.3	448	20	US-09-662-786-340	Sequence 340, App
33	186	9.3	448	20	US-09-670-568B-3	Sequence 3, Appli
34	186	9.3	448	20	US-09-685-696-340	Sequence 340, App
35	186	9.3	448	21	US-09-735-705-340	Sequence 340, App
36	186	9.3	448	22	US-09-850-716-340	Sequence 340, App
37	186	9.3	448	22	US-09-897-778-340	Sequence 340, App
38	186	9.3	516	15	US-09-174-493-14	Sequence 14, Appli
39	186	9.3	516	19	US-09-542-615A-344	Sequence 344, App
40	186	9.3	516	20	US-09-606-421A-344	Sequence 344, App
41	186	9.3	516	20	US-09-630-940A-344	Sequence 344, App
42	186	9.3	516	20	US-09-630-940B-344	Sequence 344, App
43	186	9.3	516	20	US-09-643-597-344	Sequence 344, App
44	186	9.3	516	20	US-09-662-786-344	Sequence 344, App
45	186	9.3	516	20	US-09-670-568B-344	Sequence 344, App

ALIGNMENTS

RESULT 1
PCT-US00-06602-2
; Sequence 2, Application PC/TUS00006602
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences
; CURRENT APPLICATION NUMBER: PCT/US00/06602
; CURRENT FILING DATE: 2000-03-15
; EARLIER APPLICATION NUMBER: EX99-001
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
PCT-US00-06602-2

Query Match 100.0%; Score 2008; DB 1; Length 385;
Best Local Similarity 100.0%; Pred. No. 7.4e-192;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MYISQPMWSWKSTSEDDSDSTEVDIKEDIPKTFVSGSELTPMAFLQGLNSGLMQFS	60
Db	1	MYISQPMWSWKSTSEDDSDSTEVDIKEDIPKTFVSGSELTPMAFLQGLNSGLMQFS	60
QY	61	QQSVLREMLQDIQIQAANTLPKLEHNHNGGCFSMVLDEPPKSLWYSIPLNKLIRMNK	120
Db	61	QQSVLREMLQDIQIQAANTLPKLEHNHNGGCFSMVLDEPPKSLWYSIPLNKLIRMNK	120

QY 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRCONHLSVEPLTANNAKMRESLLRSE 180
Db 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRCONHLSVEPLTANNAKMRESLLRSE 180
QY 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSTRSGLTRQTLAFKFVCQNSCIGRKETS LV 240
Db 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSTRSGLTRQTLAFKFVCQNSCIGRKETS LV 240
QY 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
Db 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
QY 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEMIKAAAAEVL R 360
Db 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEMIKAAAAEVL R 360
QY 361 NPNQENLRRHANKLLSLKKRAYELP 385
Db 361 NPNQENLRRHANKLLSLKKRAYELP 385

RESULT 2
PCT-US00-06602A-2
; Sequence 2, Application PC/TUS00006602A
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences
; CURRENT APPLICATION NUMBER: PCT/US00/06602A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EX99-001
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
PCT-US00-06602A-2

Query Match 100.0%; Score 2008; DB 1; Length 385;
Best Local Similarity 100.0%; Pred. No. 7.4e-192;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYISQPMSPWHKESTDEDDSTEVDIKEDIPKTVESGSELTPMAFLQGLNSGNLMQFS 60
Db 1 MYISQPMSPWHKESTDEDDSTEVDIKEDIPKTVESGSELTPMAFLQGLNSGNLMQFS 60
QY 61 QQSVLREMLQDIQIQTANTLPKLEHNIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
Db 61 QQSVLREMLQDIQIQTANTLPKLEHNIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
QY 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRCONHLSVEPLTANNAKMRESLLRSE 180
Db 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRCONHLSVEPLTANNAKMRESLLRSE 180
QY 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSTRSGLTRQTLAFKFVCQNSCIGRKETS LV 240
Db 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSTRSGLTRQTLAFKFVCQNSCIGRKETS LV 240
QY 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
Db 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
QY 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEMIKAAAAEVL R 360
Db 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEMIKAAAAEVL R 360
QY 361 NPNQENLRRHANKLLSLKKRAYELP 385
Db 361 NPNQENLRRHANKLLSLKKRAYELP 385

RESULT 3
US-09-268-969-2
; Sequence 2, Application US/09268969
; GENERAL INFORMATION:
; APPLICANT: Buchman, Andrew R.
; APPLICANT: Platt, Darren M.
; APPLICANT: Oilmann, Michael M.
; APPLICANT: Young, Lynn M.
; APPLICANT: Demsky, Madelyn R.
; APPLICANT: Keegan, Kevin P.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER TUMOR
; FILE REFERENCE: 7326-084
; CURRENT APPLICATION NUMBER: US/09/268,969
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-268-969-2

Query Match 100.0%; Score 2008; DB 16; Length 385;
Best Local Similarity 100.0%; Pred. No. 7.4e-192;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYISQPMSPWHKESTDEDDSTEVDIKEDIPKTVESGSELTPMAFLQGLNSGNLMQFS 60
Db 1 MYISQPMSPWHKESTDEDDSTEVDIKEDIPKTVESGSELTPMAFLQGLNSGNLMQFS 60
QY 61 QQSVLREMLQDIQIQTANTLPKLEHNIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
Db 61 QQSVLREMLQDIQIQTANTLPKLEHNIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
QY 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRCONHLSVEPLTANNAKMRESLLRSE 180
Db 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRCONHLSVEPLTANNAKMRESLLRSE 180
QY 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSTRSGLTRQTLAFKFVCQNSCIGRKETS LV 240
Db 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSTRSGLTRQTLAFKFVCQNSCIGRKETS LV 240
QY 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
Db 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
QY 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEMIKAAAAEVL R 360
Db 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEMIKAAAAEVL R 360
QY 361 NPNQENLRRHANKLLSLKKRAYELP 385
Db 361 NPNQENLRRHANKLLSLKKRAYELP 385

RESULT 4
US-09-524-101-2
; Sequence 2, Application US/09524101
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: insect p53 EX00-015
; CURRENT APPLICATION NUMBER: US/09/524,101
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 09/268,969
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/184,373
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-524-101-2

Query Match      100.0%; Score 2008; DB 19; Length 385;
Best Local Similarity 100.0%; Pred. No. 7.4e-192;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   |||||||
Db 1 MYISQPMWHKSTDEDDSTEVDIKEDIPKTVVSG:ELTTEPMFLQGLNSGNLMQFS 60
   |||||||

QY 61 QQSVLREMLQDIQIQANTLPKLENNHIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
   |||||||
Db 61 QQSVLREMLQDIQIQANTLPKLENNHIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
   |||||||

QY 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKMRESLLRSE 180
   |||||||
Db 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKMRESLLRSE 180
   |||||||

QY 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLV 240
   |||||||
Db 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLV 240
   |||||||

QY 241 FCLEKACGDIVGQHVHVHVKICTCPKRDRIQDERQLNSKKRSVPEAAEEDPEPSKVRRCIA 300
   |||||||
Db 241 FCLEKACGDIVGQHVHVHVKICTCPKRDRIQDERQLNSKKRSVPEAAEEDPEPSKVRRCIA 300
   |||||||

QY 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKWELLQSIIEGMIKEAAAEVLR 360
   |||||||
Db 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKWELLQSIIEGMIKEAAAEVLR 360
   |||||||

QY 361 NPNQENLRRHANKLLSLKKR 385
   |||||||
Db 361 NPNQENLRRHANKLLSLKKR 385
   |||||||

RESULT 5
US-60-167-217-22998
; Sequence 22998, Application US/60167217
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000152
; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22998
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Drosophila
US-60-167-217-22998

Query Match      98.3%; Score 1973; DB 24; Length 381;
Best Local Similarity 99.5%; Pred. No. 2.4e-188;
Matches 378; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYISQPMWHKSTDEDDSTEVDIKEDIPKTVVSGSELTTTEPMFLQGLNSGNLMQFS 60
   |||||||
Db 1 MYISQPMWHKSTDEDDSTEVDIKEDIPKTVVSGSELTTTEPMFLQGLNSGNLMQFS 60
   |||||||

QY 61 QQSVLREMLQDIQIQANTLPKLENNHIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
   |||||||
Db 61 QQSVLREMLQDIQIQANTLPKLENNHIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
   |||||||

QY 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKMRESLLRSE 180
   |||||||
Db 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKMRESLLRSE 180
   |||||||

QY 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLV 240
   |||||||
Db 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLV 240
   |||||||

QY 241 FCLEKACGDIVGQHVHVHVKICTCPKRDRIQDERQLNSKKRSVPEAAEEDPEPSKVRRCIA 300
   |||||||
Db 241 FCLEKACGDIVGQHVHVHVKICTCPKRDRIQDERQLNSKKRSVPEAAEEDPEPSKVRRCIA 300
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QY 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKWELLQSIIEGMIKEAAAEVLR 360
   |||||||
Db 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKWELLQSIIEGMIKEAAAEVLR 360
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QY 361 NPNQENLRRHANKLLSLKKR 385
   |||||||
Db 361 NPNQENLRRHANKLLSLKKR 385
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Db 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKMRESLLRSE 180
   |||||||

QY 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLV 240
   |||||||
Db 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLV 240
   |||||||

QY 241 FCLEKACGDIVGQHVHVHVKICTCPKRDRIQDERQLNSKKRSVPEAAEEDPEPSKVRRCIA 300
   |||||||
Db 241 FCLEKACGDIVGQHVHVHVKICTCPKRDRIQDERQLNSKKRSVPEAAEEDPEPSKVRRCIA 300
   |||||||

QY 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKWELLQSIIEGMIKEAAAEVLR 360
   |||||||
Db 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKWELLQSIIEGMIKEAAAEVLR 360
   |||||||

QY 361 NPNQENLRRHANKLLSLKKR 380
   |||||||
Db 361 NPNQENLRRHANKLLSLKSK 380
   |||||||

RESULT 6
US-60-171-625-450
; Sequence 450, Application US/60171625
; GENERAL INFORMATION:
; APPLICANT: Skupski, Marian
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS THAT SHOW
; TITLE OF INVENTION: HIGH HOMOLOGY TO KNOWN HUMAN DISEASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000179
; CURRENT APPLICATION NUMBER: US/60/171,625
; CURRENT FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 450
; LENGTH: 381
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-171-625-450

Query Match      98.3%; Score 1973; DB 24; Length 381;
Best Local Similarity 99.5%; Pred. No. 2.4e-188;
Matches 378; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYISQPMWHKSTDEDDSTEVDIKEDIPKTVVSGSELTTTEPMFLQGLNSGNLMQFS 60
   |||||||
Db 1 MYISQPMWHKSTDEDDSTEVDIKEDIPKTVVSGSELTTTEPMFLQGLNSGNLMQFS 60
   |||||||

QY 61 QQSVLREMLQDIQIQANTLPKLENNHIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
   |||||||
Db 61 QQSVLREMLQDIQIQANTLPKLENNHIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
   |||||||

QY 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKMRESLLRSE 180
   |||||||
Db 121 AFNVDVQFKSKMPIQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKMRESLLRSE 180
   |||||||

QY 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLV 240
   |||||||
Db 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLV 240
   |||||||

QY 241 FCLEKACGDIVGQHVHVHVKICTCPKRDRIQDERQLNSKKRSVPEAAEEDPEPSKVRRCIA 300
   |||||||
Db 241 FCLEKACGDIVGQHVHVHVKICTCPKRDRIQDERQLNSKKRSVPEAAEEDPEPSKVRRCIA 300
   |||||||

QY 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKWELLQSIIEGMIKEAAAEVLR 360
   |||||||
Db 301 IKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKWELLQSIIEGMIKEAAAEVLR 360
   |||||||

QY 361 NPNQENLRRHANKLLSLKKR 380
   |||||||
Db 361 NPNQENLRRHANKLLSLKSK 380
   |||||||
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```

RESULT      7
US-60-173-464-18653
; Sequence 18653, Application US/60173464
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W.D.
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000173
; CURRENT APPLICATION NUMBER: US/60/173,464
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 30269
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18653
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Drosophila
US-60-173-464-18653

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Query Match	98.3%;	Score 1973;	DB 24;	Length 381;
Best Local Similarity	99.5%;	Pred. No. 2.4e-188;		
Matches 378;	Conservative	1;	Mismatches 1;	Indels 0;
				Gaps 0;

QY	1	MYISQPM5WHKESTDESDSTEVDIKEDIPKTVESGSELTPTEPNAFLQGLNSGNIHQFS	60
Db	1	MYISQPM5WHKESTDESDSTEVDIKEDIPKTVESGSELTPTEPNAFLQGLNSGNIHQFS	60
QY	61	QQSVLREMMLQDIIQIANTLPKLENNHIGGYCF5MVLDEPPKSLMY5IPLNKLIRMNK	120
Db	61	QQSVLREMMLQDIIQIANTLPKLENNHIGGYCF5MVLDEPPKSLMY5IPLNKLIRMNK	120
QY	121	AFNVDYQFKSKMPIQPLNLRVFLCF5NDVSAPVVRCONHLSVEPLTANNAKMRESLLRSE	180
Db	121	AFNVDYQFKSKMPIQPLNLRVFLCF5NDVSAPVVRCONHLSVEPLTANNAKMRESLLRSE	180
QY	181	NPN5VYCGNAQKGISERFSVVVPLNMRSVTR5GLTRQTLAFKFVQNSCIGRKETSLV	240
Db	181	NPN5VYCGNAQKGISERFSVVVPLNMRSVTR5GLTRQTLAFKFVQNSCIGRKETSLV	240
QY	241	FCLEKACGDIVGQHVHVKICTCPKRDRIQDERQNL5KKRKS\PEAAEEDPSKVRRCIA	300
Db	241	FCLEKACGDIVGQHVHVKICTCPKRDRIQDERQNL5KKRKS\PEAAEEDPSKVRRCIA	300
QY	301	IKTEDTESNDSRDCDD5AAEWNVSRTPDGDYRLAITCPNKEA.LQ5IEGMIKEAAAAEVL	360
Db	301	IKTEDTESNDSRDCDD5AAEWNVSRTPDGDYRLAITCPNKEA.LQ5IEGMIKEAAAAEVL	360
QY	361	NPNQENLRRHANKLL5LKKR	380
Db	361	NPNQENLRRHANKLL5LKKR	380

```

RESULT      8
US-60-191-637-22730
; Sequence 22730, Application US/601916.7
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 42660
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22730
; LENGTH: 381
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-191-637-22730

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```

Query Match          98.3%; Score 1973; DB 24; Length 381;
Best Local Similarity 99.5%; Pred. No. 2.4e-188;
Matches 378; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYISQPMWHKESTDSEDDSTVEDIKEDIPKTVESGSELTTEPMAFLOGLNSGMLMQFS 60
    |||||||
Db 1 MYISQPMWHKESTDSEDDSTVEDIKEDIPKTVESGSELTTEPMAFLOGLNSGMLMQFS 60
    |||||||

QY 61 QQSVLREMMLQDIIQIQTANTLPKLEHNHIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
    |||||||
Db 61 QQSVLREMMLQDIIQIQTANTLPKLEHNHIGGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNK 120
    |||||||

QY 121 AFNVDVQFKSKMPIQIPLNLRVFLCFSDNDVSAPVVRCQNHLVSVEPLTANNAKMRESLLRSE 180
    |||||||
Db 121 AFNVDVQFKSKMPIQIPLNLRVFLCFSDNDVSAPVVRCQNHLVSVEPLTANNAKMRESLLRSE 180
    |||||||

QY 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTROTFLAFKFVCQNSCIGRKETSLV 240
    |||||||
Db 181 NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTROTFLAFKFVCQNSCIGRKETSLV 240
    |||||||

QY 241 FCLEKACGDIVGQHVHVHKICTCPKRDRIQDERQLNSKKRKSVPVEAAEEDPSKVRRCIA 300
    |||||||
Db 241 FCLEKACGDIVGQHVHVHKICTCPKRDRIQDERQLNSKKRKSVPVEAAEEDPSKVRRCIA 300
    |||||||

QY 301 IKTTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIIEGMIKEAAAEVLR 360
    |||||||
Db 301 IKTTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIIEGMIKEAAAEVLR 360
    |||||||

QY 361 NPNQENLRRHANKLLSLKKR 380
    |||||||
Db 361 NPNQENLRRHANKLLSLKSK 380
    |||||||

```

```

RESULT          9
US-60-191-681-17942
; Sequence 17942, Application US/60191681
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
; TITLE OF INVENTION: USES THEREOF.
; FILE REFERENCE: cl000390
; CURRENT APPLICATION NUMBER: US/60/191,681
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 30973
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17942
; LENGTH: 381
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-191-681-17942

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Query Match	98.3%;	Score 1973;	DB 24;	Length 381;
Best Local Similarity	99.5%;	Pred. No. 2.4e-188;		
Matches 378;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MYISQPSMWHKESTDSEDDSTEVDIKEDIPKTVGVSGSELTTTEPMAFLOGLNSGNLMQFS	60	
Db	1	MYISQPSMWHKESTDSEDDSTEVDIKEDIPKTVGVSGSELTTTEPMAFLOGLNSGNLMQFS	60	
QY	61	QOSVLRREMLQDIQIQAANTLPKLEHNIGGYCFSMVLDEPPKSLWMYSIPLNKLIRMNK	120	
Db	61	QOSVLRREMLQDIQIQAANTLPKLEHNIGGYCFSMVLDEPPKSLWMYSIPLNKLIRMNK	120	
QY	121	AFNVDVQFKSKMPIQPLNLRVFLCFSDNVSAPVVRQCNHLSVEPLTANNAKMRESLLRSE	180	
Db	121	AFNVDVQFKSKMPIQPLNLRVFLCFSDNVSAPVVRQCNHLSVEPLTANNAKMRESLLRSE	180	
QY	181	NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKPVQCNSCIGRKETS LV	240	
Db	181	NPNSVYCGNAQKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKPVQCNSCIGRKETS LV	240	

QY 241 FCLEKACGDIVGQHVHVKICTCPKRDRIQDEROLNSKKRSVPEAAEEDEPSKVRRCIA 300
Db 241 FCLEKACGDIVGQHVHVKICTCPKRDRIQDEROLNSKKRSVPEAAEEDEPSKVRRCIA 300
QY 301 IKTEDESNDSDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEGMIKEAAAEVLR 360
Db 301 IKTEDESNDSDCDDSAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEGMIKEAAAEVLR 360
QY 361 NPNQENLRHANKLLSLKKR 380
Db 361 NPNQENLRHANKLLSLKSK 380

RESULT 10
PCT-US00-06602-4
; Sequence 4, Application PC/TUS00006602
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences
; CURRENT APPLICATION NUMBER: PCT/US00/06602
; CURRENT FILING DATE: 2000-03-15
; EARLIER APPLICATION NUMBER: EX99-001
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Leptinotarsa decemlineata
PCT-US00-06602-4

Query Match 15.0%; Score 300.5; DB 1; Length 354;
Best Local Similarity 28.5%; Pred. No. 1.1e-20;
Matches 103; Conservative 60; Mismatches 122; Indels 77; Gaps 18;

QY 45 MAFLOGLNSGNLMQFSQQSVLREMLQDI---QIQAN-----TLPKLENH 86
Db 17 LAEMEGDNMDNLFNFFKDEPTLNDLNSYLNGSIVANDDSKMVHLIFPGVQTSVPSNDEY 76
QY 87 NIGGYCFSMVLDEPP---KSLWMYSIPLNKLKLYIRMNKAFFNVDVQFKSKMPIQLNLRVFL 143
Db 77 D-GPYEFE--VDVHPTVAKNSWVYSTTLNKVYMTGSPFPVDFRV-SHRPPNPLFIR--- 129
QY 144 CFSNDV-SAP-----VVRCQNHLVSVEPLTANNAK--MRESLLRSENPNNSVYCGNAGKG 194
Db 130 --STPVYSAPOFAQECVYRCLNHEFSKESDGLKEHIRPHIIRCANQYAAAYLGD---KS 184
QY 195 ISERFSVVPLNMSRVSRTSGLTRQTLAFKFCVQNSC----IGRKETSLVFCLEKACGDI 250
Db 185 KNERLSVVIPIPGIPQTGTES--VRE--IFEVCKNSCPSGPMNRRRAVEIIFTLEDNQGTI 240
QY 251 VGOHVHVKICTCPKRDRIQDE-----RQLNSKKRSKSVPEAAEEDEPSKVR 296
Db 241 YGRKTLNVRICSCPKRDKKDEKDNANTNLPHGKKRKMESPSKKPMQTQAEND-TKEFT 299
QY 297 RCIAKTEDESNDSDCDDSAAE---WNVSRTPDGDYRLAITCPNKEWLLQSIEGMIKE 353
Db 300 LTIPLVGRHNEQNVLYKCHDLMAEILRNIGNGTEGPKYKIA-----LNKINTLIRE 350
QY 354 AA 355
Db 351 SS 352

RESULT 11
PCT-US00-06602A-4
; Sequence 4, Application PC/TUS00006602A
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences

; CURRENT APPLICATION NUMBER: PCT/US00/06602A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EX99-001
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Leptinotarsa decemlineata
PCT-US00-06602A-4

Query Match 15.0%; Score 300.5; DB 1; Length 354;
Best Local Similarity 28.5%; Pred. No. 1.1e-20;
Matches 103; Conservative 60; Mismatches 122; Indels 77; Gaps 18;
QY 45 MAFLOGLNSGNLMQFSQQSVLREMLQDI---QIQAN-----TLPKLENH 86
Db 17 LAEMEGDNMDNLFNFFKDEPTLNDLNSYLNGSIVANDDSKMVHLIFPGVQTSVPSNDEY 76
QY 87 NIGGYCFSMVLDEPP---KSLWMYSIPLNKLKLYIRMNKAFFNVDVQFKSKMPIQLNLRVFL 143
Db 77 D-GPYEFE--VDVHPTVAKNSWVYSTTLNKVYMTGSPFPVDFRV-SHRPPNPLFIR--- 129
QY 144 CFSNDV-SAP-----VVRCQNHLVSVEPLTANNAK--MRESLLRSENPNNSVYCGNAGKG 194
Db 130 --STPVYSAPOFAQECVYRCLNHEFSKESDGLKEHIRPHIIRCANQYAAAYLGD---KS 184
QY 195 ISERFSVVPLNMSRVSRTSGLTRQTLAFKFCVQNSC----IGRKETSLVFCLEKACGDI 250
Db 185 KNERLSVVIPIPGIPQTGTES--VRE--IFEVCKNSCPSGPMNRRRAVEIIFTLEDNQGTI 240
QY 251 VGOHVHVKICTCPKRDRIQDE-----RQLNSKKRSKSVPEAAEEDEPSKVR 296
Db 241 YGRKTLNVRICSCPKRDKKDEKDNANTNLPHGKKRKMESPSKKPMQTQAEND-TKEFT 299
QY 297 RCIAKTEDESNDSDCDDSAAE---WNVSRTPDGDYRLAITCPNKEWLLQSIEGMIKE 353
Db 300 LTIPLVGRHNEQNVLYKCHDLMAEILRNIGNGTEGPKYKIA-----LNKINTLIRE 350

QY 354 AA 355
Db 351 SS 352

RESULT 12
US-09-524-101-4
; Sequence 4, Application US/09524101
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 EX00-015
; CURRENT APPLICATION NUMBER: US/09/524,101
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 09/268,969
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/184,373
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Leptinotarsa decemlineata
US-09-524-101-4

Query Match 15.0%; Score 300.5; DB 19; Length 354;
Best Local Similarity 28.5%; Pred. No. 1.1e-20;
Matches 103; Conservative 60; Mismatches 122; Indels 77; Gaps 18;
QY 45 MAFLOGLNSGNLMQFSQQSVLREMLQDI---QIQAN-----TLPKLENH 86

Db 17 LAEMEGDNMDLNFFKDEPTLNDLNSNILNGSIVANDDSKMVHLIFPGVQTSVPSNDEY 76
QY 87 NIGGYCFSMVLDEPP---KSLWMSYIPLNKLIRMNKAFNVDVQFKSKMPIQLNLRVFL 143
Db 77 D-GPYEFE--VDVHTVAKNSWVYSTTLNKVYMTMGSPFPVDFRV-SHRPPNPLFIR--- 129
QY 144 CFSNDV-SAP-----VVRQCNHLSVEPLTANNAK--MRESLLRSENPNNSVYCGNAQKG 194
Db 130 --STPVYSAQFAQECVYRCLNHEFSHKESDGLKEHIRPHIRCANQYAYLGD--KS 184
QY 195 ISERFSVVVPLNMSRVSRTSLRQTLAFKFCVQNSC----IGRKETSLVFCLEKACGDI 250
Db 185 KNERLSVVIPIGIPQTGES--VRE--IFEVCKNSCSPSPGMNRRRAVEIITLEDNQGTI 240
QY 251 VGOHVHVKICTCPKRDRIQDE-----RQLNSKKRKSVPAAAEDEPSKVR 296
Db 241 YGRKTLNVRICSPKRDKEKDEKDNANTNLPHGKKRKMKEPSSKPMQTAEND-TKEFT 299
QY 297 RCIAIKTEDTESNDSRDCDDSAAB---WNVSRTPDGDYRLAITCPNKEWLLQSIEMIKE 353
Db 300 LTIPLVGRHNEQNVLYKCHDLMAGEILRNIGNTEGPKYKIA-----LNKINTLIRE 350
QY 354 AA 355
Db 351 SS 352

RESULT 13
PCT-US00-06602-6
; Sequence 6, Application PC/TUS00006602
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences
; CURRENT APPLICATION NUMBER: PCT/US00/06602
; CURRENT FILING DATE: 2000-03-15
; EARLIER APPLICATION NUMBER: EX99-001
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Tribolium castaneum
PCT-US00-06602-6

Query Match 12.3%; Score 247.5; DB 1, Length 350;
Best Local Similarity 24.2%; Pred. No. 2.3e-15;
Matches 88; Conservative 67; Mismatches 124; Indels 85; Gaps 17;
QY 25 IKEDIPKTVESGSELTEPMAFLQGLNSGMLMOPFSQSVLREMML---QDIQIQUANTLP 81
Db 23 LKDDVGRIMHNNVHLVND-----DGEEEKYSNEANYTESIFPPDQPTNLGTEEYP 73
QY 82 KLENHNIGGYCFSMVLD-EPPKSLWMSYIPLNKLIRMNKAFNVDVQFKSKMPIQLNLR 140
Db 74 -----GPFNFSVLISPNEQKSPWEYSEKLNKIFIGINVKFPVAFSVQNRPNQPLYIR 126
QY 141 VFLCFS-----NDVSAPVVRQCNHLSVEPLTANNAKMR---ESLLRSENPNNSVYCGNAQ 191
Db 127 ATPVFSQTHFQDL---VHRCVGRH--HPQDQSNKGVAPHIFQHIIRCTNDNALYFGD-- 179
QY 192 GKGISERFSVVVPL---NMSRSVTRSGLTRQTLAFKFCVQNSC---IGRKETSLVFCLEK 245
Db 180 -KNTGTRLNIVLPLAHPQVGEDVVKE-----FFQFVCKNSCPLGMNRRPIDVVFTLED 231
QY 246 ACQDIVGQHVHVKICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIAIKTED 305
Db 127 ATPVFSQTHFQDL---VHRCVGRH--HPQDQSNKGVAPHIFQHIIRCTNDNALYFGD-- 179
QY 192 GKGISERFSVVVPL---NMSRSVTRSGLTRQTLAFKFCVQNSC---IGRKETSLVFCLEK 245
Db 180 -KNTGTRLNIVLPLAHPQVGEDVVKE-----FFQFVCKNSCPLGMNRRPIDVVFTLED 231
QY 246 ACQDIVGQHVHVKICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIAIKTED 305
Db 232 NKEVEGRRRLVGRVVCSPKRDKEEDMES-----AVP-----PRRKRKL----- 274
QY 306 TESNDSRDCDDSAAEWNVSRTPDGD-----YRLAITCPNKEWLLQSIEMIKEAAAEVLR 360

Db 275 --GNDERRV-----VPQSSDNKIFALNIHIPGKNYLOALKMCQDMLANEILK 321
QY 361 NPNQ 364
Db 322 KQEQ 325
RESULT 14
PCT-US00-06602A-6
; Sequence 6, Application PC/TUS00006602A
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences
; CURRENT APPLICATION NUMBER: PCT/US00/06602A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EX99-001
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Tribolium castaneum
PCT-US00-06602A-6

Query Match 12.3%; Score 247.5; DB 1, Length 350;
Best Local Similarity 24.2%; Pred. No. 2.3e-15;
Matches 88; Conservative 67; Mismatches 124; Indels 85; Gaps 17;
QY 25 IKEDIPKTVESGSELTEPMAFLQGLNSGMLMOPFSQSVLREMML---QDIQIQUANTLP 81
Db 23 LKDDVGRIMHNNVHLVND-----DGEEEKYSNEANYTESIFPPDQPTNLGTEEYP 73
QY 82 KLENHNIGGYCFSMVLD-EPPKSLWMSYIPLNKLIRMNKAFNVDVQFKSKMPIQLNLR 140
Db 74 -----GPFNFSVLISPNEQKSPWEYSEKLNKIFIGINVKFPVAFSVQNRPNQPLYIR 126
QY 141 VFLCFS-----NDVSAPVVRQCNHLSVEPLTANNAKMR---ESLLRSENPNNSVYCGNAQ 191
Db 127 ATPVFSQTHFQDL---VHRCVGRH--HPQDQSNKGVAPHIFQHIIRCTNDNALYFGD-- 179
QY 192 GKGISERFSVVVPL---NMSRSVTRSGLTRQTLAFKFCVQNSC---IGRKETSLVFCLEK 245
Db 180 -KNTGTRLNIVLPLAHPQVGEDVVKE-----FFQFVCKNSCPLGMNRRPIDVVFTLED 231
QY 246 ACQDIVGQHVHVKICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIAIKTED 305
Db 232 NKEVEGRRRLVGRVVCSPKRDKEEDMES-----AVP-----PRRKRKL----- 274
QY 306 TESNDSRDCDDSAAEWNVSRTPDGD-----YRLAITCPNKEWLLQSIEMIKEAAAEVLR 360
Db 275 --GNDERRV-----VPQSSDNKIFALNIHIPGKNYLOALKMCQDMLANEILK 321
QY 361 NPNQ 364
Db 322 KQEQ 325
RESULT 15
US-09-524-101-6
; Sequence 6, Application US/09524101
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 EX00-015
; CURRENT APPLICATION NUMBER: US/09/524,101
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 09/268,969
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/184,373

Search completed: November 16, 2001, 15:55:05
Job time: 472 sec

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OM protein - protein search, using sw model

Run on: November 16, 2001, 15:48:48 ; Search time 46.31 Seconds
(without alignments)
44 261 Million cell updates/sec

Title: US-09-524-101-2
Perfect score: 2008
Sequence: 1 MYISQPMWHKESTDSEDDSS.....NLRHANKLLSLKKRAYELP 385

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 25203 seqs, 5323989 residues

Total number of hits satisfying chosen parameters: 25203

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/pct_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	9.3	448	5 US-09-850-716A-34	Sequence 340, App
2	186	9.3	516	5 US-09-850-716A-37	Sequence 344, App
3	186	9.3	641	5 US-09-850-716A-37	Sequence 339, App
4	186	9.3	680	5 US-09-850-716A-34	Sequence 342, App
5	179	8.9	586	5 US-09-850-716A-152	Sequence 152, App
6	178	8.9	356	5 US-09-850-716A-341	Sequence 341, App
7	178	8.9	461	5 US-09-850-716A-343	Sequence 343, App
8	178	8.9	586	5 US-09-850-716A-338	Sequence 338, App
9	98.5	4.9	645	5 US-09-609-360C-15	Sequence 15, Appl
10	98.5	4.9	645	5 US-09-609-360C-16	Sequence 16, Appl
11	98.5	4.9	645	5 US-09-345-473E-15	Sequence 15, Appl
12	98.5	4.9	645	5 US-09-345-473E-16	Sequence 16, Appl
13	96	4.8	604	5 US-09-609-360C-17	Sequence 17, Appl
14	96	4.8	604	5 US-09-345-473E-17	Sequence 17, Appl
15	91.5	4.6	347	5 US-09-816-028A-17	Sequence 17, Appl
16	85	4.2	1401	5 US-09-976-594-1035	Sequence 1035, Ap
17	80	4.0	1369	1 PCT-US01-09369-42	Sequence 42, Appl
18	79.5	4.0	219	1 PCT-US01-31656-3	Sequence 3, Appli
19	79	3.9	434	1 PCT-US01-17103-14	Sequence 14, Appl
20	78.5	3.9	667	5 US-09-815-242-12811	Sequence 12811, A
21	77.5	3.9	237	5 US-09-897-516-6135	Sequence 6135, Ap
22	75	3.7	582	5 US-09-848-909-28	Sequence 28, Appl
23	75	3.7	721	5 US-09-848-909-34	Sequence 34, Appl
24	74.5	3.7	657	5 US-09-815-242-5408	Sequence 5408, Ap
25	74.5	3.7	667	5 US-09-815-242-12490	Sequence 12490, A
26	73	3.6	422	5 US-09-815-242-11825	Sequence 11825, A
27	72	3.6	240	5 US-09-974-298-147	Sequence 147, App

28	72	3.6	879	5 US-09-659-287A-2	Sequence 2, Appli
29	72	3.6	1388	5 US-09-976-594-296	Sequence 296, App
30	71.5	3.6	858	5 US-09-815-242-11396	Sequence 11396, A
31	71.5	3.6	1167	5 US-09-803-671B-2	Sequence 2, Appli
32	71	3.5	227	5 US-09-897-516-6293	Sequence 6293, Ap
33	71	3.5	447	5 US-09-897-516-5688	Sequence 5688, Ap
34	71	3.5	618	5 US-09-897-516-6662	Sequence 6662, Ap
35	71	3.5	855	5 US-09-900-751-2	Sequence 2, Appli
36	70.5	3.5	247	5 US-09-981-353-95	Sequence 95, Appl
37	70.5	3.5	255	5 US-09-973-278-386	Sequence 386, App
38	70.5	3.5	465	5 US-09-969-515-12	Sequence 12, Appl
39	70.5	3.5	476	5 US-09-969-515-6	Sequence 6, Appli
40	70.5	3.5	844	5 US-09-815-242-13515	Sequence 13515, A
41	70.5	3.5	969	5 US-09-969-515-10	Sequence 10, Appl
42	70.5	3.5	980	5 US-09-969-515-4	Sequence 4, Appli
43	70.5	3.5	1213	5 US-09-969-515-8	Sequence 8, Appli
44	70.5	3.5	1224	5 US-09-969-515-2	Sequence 2, Appli
45	70	3.5	227	5 US-09-897-516-5947	Sequence 5947, Ap

ALIGNMENTS

RESULT 1
US-09-850-716A-340
; Sequence 340, Application US/09850716A
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-340

Query Match	9.3%	Score 186;	DB 5;	Length 448;
Best Local Similarity	22.2%	Pred. No. 2.5e-10;		
Matches	75;	Conservative	59;	Mismatches 124; Indels 80; Gaps 15;
QY	5	QPMWHKESTDSEDDST-EVDIKEDIPKTVESGSELTTEPMAFLQGLNSGNLMQFSQQS	63	
Db	31	QPIDLNFVDEPSEGDGATNKIEISMD--CIRQDSDL-SDPM-----WPQYTNLG	76	
QY	64	VLREMMLODIQIQ---ANTLPKLENH-----NI	88	
Db	77	LLNSM---DQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSTNDYP	133	
QY	89	GGYCFSMVLDE---PPKSLWMSIPLNKLYIRNKAFNVQVQFKSKMPIQPINLRVFLCF	145	
Db	134	GPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY	192	
QY	146	--SNDVSAPVVRCONHLSVEPLTANNNAKMRSELLRSENPNVYCGNAQKGISE----	199	
Db	193	KKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ	245	
QY	200	SVVPLNMSRSVTRSGLTRQTAFKFCVQNSCIG---RKETSIVFCLEKACGDIVGQHV	256	
Db	246	SVLVFY---EPPQVGTEFTVLYNFMCSVCGMRRRPIILVITLETTRDQVIGRRCF	301	
QY	257	HVKICTCPKRDRIQDERQLNSKKRKSVPAAEEDPSK	294	
Db	302	EARICACPRDRKADE---DSIRKQOVSDTKNGDGTK	336	

```
Matches      75;   Conservative     59; Mismatches    124; Indels       80; Gaps        15
```

```
QY      5 QPMSWHKESTDSEDDST-EVDIKEDIPKTVESGSELTEPEMAFLQLNSGNLMQFSQQS 63  
|| : ||| : |::| | : : |:| ::||  
Db      31 QPIDLNFVDEPSDGTATNIEISMD---CIRMQSDSL-SDPM-----WPQYTNLG 76  
  
QY      64 VLREMLLDIQIQA--ANTLPKLENH-----NI 88  
:| | | | | | | :| | | |:  
Db      77 LLNSM---DQIQNGSSSTSPYNTDHAQNVSAPTAPYAQPSTFDALSPAIPSNTDYP 133  
  
QY      89 GGCFCSMVLE---PPKSLLWMSIPLNKLYIRMNKAFFNDVVQFKSKMPIQLPLNRVLFCF 145  
| : | : : : : : | | | | | | | : : : | | : |:  
Db      134 GPSDFDSVFQSSTAQSATAWTYSTELKKLYCIAKTCTPIQIKVMTPPP-QGAIVRAMPVY 192  
  
QY      146 --SNDVDAPVRCONHLRSVEPLTANNAKMRESLLRSENPNSVYCNAQGKGISE----RF 199  
: : | : | | | | | | | | | | | | | | | : : : |:  
Db      193 KKAHVTEVKRCPCNHLSREFNEGIAPPSHLRIVE-----GNSHAQYVEDPITGRQ 245  
  
QY      200 SVVVP LNMR S VTRSGLTQT LA FKV CONSCIG ---RKETS LV FC LEKACGD IVGHVI 256  
||:|| : : | : : : | : | : | : | | : : | : | : |:  
Db      246 SVLVPY---EPPQVGTEFTTVLFNMCMNCSSCVGGMMRRPILIIVTLET RDGV L GRRCF 301  
  
QY      257 HVKI CTCPKRDR IQDEROL NS KK R KS VP EAAEEDEPSK 294  
: || || || || || : |::| : : : | : : : |:  
Db      302 EARICACPGRDKADE---DSIRKOQVSDSTKNRGDTK 336  

```

RESULT 4

```
US-09-850-716A-342  
; Sequence 342, Application US/09850716A  
; GENERAL INFORMATION:  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Retter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 342  
; LENGTH: 680  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716A-342
```

Query Match 9.3%; Score 186; DB 5; Length 680;
Best Local Similarity 22.2%; Pred.No. 4.6e-10;

Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15

```
QY      5 QPMSWHKESTDSEDDST-EVDIKEDIPKTVESGSELTEPEMAFLQLNSGNLMQFSQQS 63  
|| : ||| : |::| | : : |:| ::||  
Db      70 QPIDLNFVDEPSDGTATNIEISMD---CIRMQSDSL-SDPM-----WPQYTNLG 115  
  
QY      64 VLREMLLDIQIQA--ANTLPKLENH-----NI 88  
:| | | | | | | :~| | | |:  
Db      116 LLNSM---DQIQNGSSSTSPYNTDHAQNVSAPTAPYAQPSTFDALSPAIPSNTDYP 172  
  
QY      89 GGCFCSMVLE---PPKSLLWMSIPLNKLYIRMNKAFFNDVVQFKSKMPIQLPLNRVLFCF 145  
| : | : : : : : | | | | | | | : : : | | : |:  
Db      173 GPSDFDSVFQSSTAQSATAWTYSTELKKLYCIAKTCTPIQIKVMTPPP-QGAIVRAMPVY 231  
  
QY      146 --SNDVDAPVRCONHLRSVEPLTANNAKMRESLLRSENPNSVYCNAQGKGISE----RF 199  
: : | : | | | | | | | | | | | | | | | : : : |:  
Db      232 KKAHVTEVKRCPCNHLSREFNEGIAPPSHLRIVE-----GNSHAQYVEDPITGRQ 284  
  
QY      200 SVVVP LNMR S VTRSGLTQT LA FKV CONSCIG ---RKETS LV FC LEKACGD IVGHVI 256  
||:|| : : | : : : | : | : | : | | : : | : | : |:  
Db      285 SVLVPY---EPPQVGTEFTTVLFNMCMNCSSCVGGMMRRPILIIVTLET RDGV L GRRCF 340  
  
QY      257 HVKI CTCPKRDR IQDEROL NS KK R KS VP EAAEEDEPSK 294
```


Db 86 LNDNFGDFPESLTLHLRLKTIFLSG---NRLSGRIPSSLLRLSRLYTLNVEDNLTGTS 142

QY 132 MPIQPLN---LRVFLCFNSDVSAPVVRQNMELQVEPLTANNAKMRESLLRSENPNSVYCG 188

Db 143 IP--PLNQTSRLRYFNVSNNKLSGQI-----PLTRALKQFDES---SFTGNVALCG 187

QY 189 NAQKGKISERFSVVVPLNMSRSVTRSGLTRQTLAPKFVCQNSCIGRKETSLSVFCLEKACG 248

Db 188 DQIGKEQSELIGII-----AG 203

QY 249 DIVGQHVIVHKICT---CPKRDRIQDERQLNSKKRSVPPEAAEEDPSKVRRCIAIKTE 304

Db 204 SVAGGVLVLLILLTLIVCWPRKR-RNQAPREDRKGKGAIAE-----GATTA 250

QY 305 DTESNDSRDCDDSAAEWNVSRTPDGYRLAI---TCPNKEWLLQ-SIEGMIKEAAAEVL- 359

Db 251 ETERDIER--KDRGFSW--ERGEEGAVGTLVFLGTSDSGETVVRVYTMEDLLK-ASAETLG 305

QY 360 -----RNPNOENLRRHANKLLSLKK-----RAY 382

Db 306 RGTGLGTYKAVMESGFIVTVKRLKNARYPRMEEFKRHVEILGQLKHPNLVPLRAY 360

RESULT 14

US-09-345-473E-17

; Sequence 17, Application US/09345473E

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin

; TITLE OF INVENTION: Novel Kinases and Uses Thereof

; FILE REFERENCE: 35800/183781

; CURRENT APPLICATION NUMBER: US/09/345,473E

; CURRENT FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 604

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-09-345-473E-17

Query Match 4.8%; Score 96; DB 5; Length 604;

Best Local Similarity 20.0%; Pred. No. 0.12;

Matches 83; Conservative 55; Mismatches 119; Indels 158; Gaps 21;

QY 38 SELTTEPMALQGLNSGMLQFSQSVLREMLQDIQIANTL---PKL----- 83

Db 34 SKLVLEYLNLGTSLNEKSLNQLDQLRVL-----SFKANSLSGSIPNLGLVNLKSVY 85

QY 84 --ENHNIGGYCFSMVLDEPPKSLMWYSIPLNKL-----YIRMKAFNVDVQ---FKSK 131

Db 86 LNDNFGDFPESLTLHLRLKTIFLSG---NRLSGRIPSSLLRLSRLYTLNVEDNLTGTS 142

QY 132 MPIQPLN---LRVFLCFNSDVSAPVVRQNHLSVEPLTANNAKMRESLLRSENPNSVYCG 188

Db 143 IP--PLNQTSRLRYFNVSNNKLSGQI-----PLTRALKQFDES---SFTGNVALCG 187

QY 189 NAQKGKISERFSVVVPLNMSRSVTRSGLTRQTLAPKFVCQNSCIGRKETSLSVFCLEKACG 248

Db 188 DQIGKEQSELIGII-----AG 203

QY 249 DIVGQHVIVHKICT---CPKRDRIQDERQLNSKKRSVPPEAAEEDPSKVRRCIAIKTE 304

Db 204 SVAGGVLVLLILLTLIVCWPRKR-RNQAPREDRKGKGAIAE-----GATTA 250

QY 305 DTESNDSRDCDDSAAEWNVSRTPDGYRLAI---TCPNKEWLLQ-SIEGMIKEAAAEVL- 359

Db 251 ETERDIER--KDRGFSW--ERGEEGAVGTLVFLGTSDSGETVVRVYTMEDLLK-ASAETLG 305

QY 360 -----RNPNOENLRRHANKLLSLKK-----RAY 382

Db 306 RGTGLGTYKAVMESGFIVTVKRLKNARYPRMEEFKRHVEILGQLKHPNLVPLRAY 360

RESULT 15

US-09-816-028A-17

; Sequence 17, Application US/09816028A

; GENERAL INFORMATION:

; APPLICANT: Gilbert, Michel

; APPLICANT: Wakarchuk, Warren W.

; APPLICANT: National Research Council of Canada

; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of

; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics

; FILE REFERENCE: 019633-000111US

; CURRENT APPLICATION NUMBER: US/09/816,028A

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/118,213

; PRIOR FILING DATE: 1999-02-01

; PRIOR APPLICATION NUMBER: US 09/495,406

; PRIOR FILING DATE: 2000-01-31

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 347

; TYPE: PRT

; ORGANISM: Campylobacter jejuni

; FEATURE:

; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)

; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)

; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)

US-09-816-028A-17

Query Match 4.6%; Score 91.5; DB 5; Length 347;

Best Local Similarity 22.5%; Pred. No. 0.14;

Matches 46; Conservative 31; Mismatches 62; Indels 65; Gaps 9;

QY 24 DIKEDIPKTVEVSGSELTTTEPMALFQGLNSGMLQFSQSVL-----R 66

Db 77 DEKSKDPKS-----PLNPWAFIRVKNEAITLKASLESILPAIQRGVIGYNDCTDGE 128

QY 67 EMLLQ-----DIQIQANTLPKLENHNIGGYCFSMVLDEPPKSLMWYSIPL 111

Db 129 EIILEFCKQYPSFIPIKYPYEQIQN---PKSEENKLYSY-YNVASFIPKDEWLKIDV 184

QY 112 NKLY--IRMNKAFNV-----DVQFKSKMPIQPLNLRVFLCFNSDVSAPVVRQNHLSVEP 164

Db 185 DHYIDAKKLYKSFYIPKNKYDVVSYSRVDIHYFNDNFFLCKDNN-----GNILKEP 235

QY 165 -----LTANNAKMRESLLRSENPN 183

Db 236 GDCLLINNYNLKWKEVLIDRINN 259

Search completed: November 16, 2001, 15:56:05

Job time: 437 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2001, 15:03:33 ; Search time 50.08 Seconds
(without alignments)
466.059 Million cell updates/sec

Title: US-09-524-101-2
Perfect score: 2008
Sequence: 1 MYISQMSWHKSTSEDDSDS.....NLRHANKLLSKRAYELP 385

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseq/AA1981.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2008	100.0	385	21 AAB00119	Dmp53 tumour suppressor
2	300.5	15.0	354	21 AAB00120	CPBP53 tumour suppressor
3	247.5	12.3	350	21 AAB00121	TRIB-Ap53 tumour suppressor
4	194	9.7	636	21 AAY50999	Human p73 protein.
5	191	9.5	499	18 AAW36190	Human p53 tumour suppressor
6	191	9.5	499	21 AAY44635	Human p73 beta splice variant
7	191	9.5	635	20 AAW30661	Human NBS-1 alpha
8	191	9.5	636	18 AAW36184	Human p53 tumour suppressor
9	191	9.5	636	21 AAY44634	Human p73 alpha splice variant
10	190	9.5	499	18 AAW36183	Monkey p53 tumour suppressor
11	190	9.5	637	18 AAW36182	Monkey p53 tumour suppressor

12	186	9.3	448	20 AAY45246	Human p51 protein
13	186	9.3	448	20 AAY05955	Human cell regulator
14	186	9.3	448	21 AAB11359	Human p63 protein
15	186	9.3	516	20 AAY05954	Human cell regulator
16	186	9.3	516	21 AAB11363	Human p63 protein
17	186	9.3	641	20 AAY45247	Human p51 protein
18	186	9.3	641	20 AAY05953	Human cell regulator
19	186	9.3	641	21 AAB11358	Human p63 protein
20	186	9.3	680	21 AAB11361	Human p63 protein
21	186	9.3	680	21 AAY50997	Human KET protein.
22	185	9.2	680	20 AAY05958	Human cell regulator
23	183	9.1	680	21 AAY50998	Rat KET protein.
24	182	9.1	461	20 AAY05963	Mouse cell regulator
25	182	9.1	586	20 AAY05962	Mouse cell regulator
26	181	9.0	483	20 AAY05961	Mouse cell regulator
27	179	8.9	586	20 AAY41032	Human lung tumor a
28	179	8.9	586	21 AAB11317	Human lung cancer-
29	178	8.9	356	20 AAY43135	Human p40 protein
30	178	8.9	356	21 AAB11360	Human p63 protein
31	178	8.9	389	20 AAY05964	Mouse cell regulator
32	178	8.9	393	20 AAY05957	Human cell regulator
33	178	8.9	461	21 AAB11362	Human p63 protein
34	178	8.9	586	20 AAY05956	Human cell regulator
35	178	8.9	586	21 AAB11357	Human p63 protein
36	171	8.5	506	18 AAW36188	Human p53 tumour s
37	171	8.5	587	18 AAW36187	Human p53 tumour s
38	171	8.5	588	18 AAW36189	Human p53 tumour s
39	170.5	8.5	390	19 AAW37998	Amino acid sequenc
40	168.5	8.4	390	19 AAW37997	Murine tumour-asso
41	168.5	8.4	390	21 AAY70786	Mouse p53 protein.
42	167.5	8.3	390	17 AAW02623	Amino acid sequenc
43	167.5	8.3	390	19 AAW48659	Chimeric p53 prote
44	166.5	8.2	370	18 AAW13957	Mouse p53 tumour s
45	165	8.2	589	18 AAW36185	

ALIGNMENTS

RESULT	1
AAB00119	
ID	AAB00119 standard; Protein: 385 AA.
XX	
AC	AAB00119;
XX	
DT	08-FEB-2001 (first entry)
XX	
DE	Dmp53 tumour suppressor polypeptide.
XX	
KW	p53; tumour suppressor gene; insect; phenotype: metazoa;
KW	invertebrate; screening; pharmaceutical; pesiticide; mis-expression;
KW	mutation; modulation.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200055178-A1.
XX	
PD	21-SEP-2000.
XX	
PF	13-MAR-2000; 2000WO-US06602.
XX	
PR	16-MAR-1999; 99US-0268969.
XX	
PA	23-FEB-2000; 2000US-0184373.
XX	
XX	(EXEL-) EXELIXIS INC.
PI	Buchman AR, Platt DM, Ollman MM, Young LM, Demsky MR, Keegan KP;
PI	Friedman L, Koczynski C, Larson JS, Robertson SA;
XX	
DR	WPI; 2000-638178/61.
DR	N-PSDB; AAA53973.
XX	
PT	Novel p53 tumor suppressor gene encoding a protein useful for

Db 300 ltipivgrhneqnvikychdlmageilrlnignptegpykia-----lnkintlire 350

QY 354 AA 355

Db 351 SS 352

RESULT 3

AAB00121

ID AAB00121 standard; Protein; 350 AA.

XX

AC AAB00121;

XX

DT 08-FEB-2001 (first entry)

XX

DE TRIB-Ap53 tumour suppressor polypeptide.

XX

XX p53; tumour suppressor gene; insect; phenotype; metazoa;

KW invertebrate; screening; pharmaceutical; pesiticide; mis-expression;

KW mutation; modulation.

XX

OS Tribolium castaneum.

XX

PN WO200055178-A1.

XX

PD 21-SEP-2000.

XX

PF 13-MAR-2000; 2000WO-US06602.

XX

PR 16-MAR-1999; 99US-0268969.

PR 23-FEB-2000; 2000US-0184373.

XX

PA (EXEL-) EXELIXIS INC.

XX

PI Buchman AR, Platt DM, Ollman MM, Young LM, Densky MR, Keegan KP;

PI Friedman L, Koczynski C, Larson JS, Robertson SA;

XX

DR WPI; 2000-638178/61.

DR N-PSDB; AAAS3975.

XX

PT Novel p53 tumor suppressor gene encoding a protein useful for

PT genetically modifying metazoan invertebrate organisms, such as insects

PT for screening compounds of pharmaceutical use or a pesticide

XX

PS Claim 14; Page 75-76; 98pp; English.

XX

CC Insect p53 tumour suppressor genes can be used to genetically modify

CC metazoan invertebrate organisms, such as insects and worms, or

CC cultured cells, resulting in p53 expression or mis-expression. The

CC tumour suppressor genes, a p53 polypeptide or genetically modified

CC organisms or cells are used in screening assays to identify compounds

CC or molecules, preferably a pharmaceutical agent or a pesticide, that

CC modulates p53 activity. The genetically modified organisms or cells

CC are also useful for studying p53 activity by detecting the phenotype

CC caused by the expression or mis-expression of the p53 protein in the

CC insect. The method additionally comprises observing a second insect

CC having the same genetic modification as the previous one, which

CC causes the expression or mis-expression of the p53 protein, where the

CC second animal additionally comprises a mutation in a desired gene and

CC differences between the phenotype of the first and second identifies

CC the desired gene as capable of modifying the function of the gene

CC encoding the p53 protein. The genetically modified organisms or

CC cells are also useful for identifying other genes modulating the

CC function of, or interaction with the p53 gene.

XX

SQ Sequence 350 AA;

Query Match 12.3%; Score 247.5; DB 21; Length 350;

Best Local Similarity 24.2%; Pred. No. 2.2e-17;

Matches 88; Conservative 67; Mismatches 124; Indels 85; Gaps 17;

QY 25 IKEDIPKTVESGSELTEPMAFLOGLNSGLMFSQSVLRMML---QDIQIQANTLP 81

Db 23 lkddvgrimhennvhlvd-----dgeekysneanytesifppdqptnlgteey 73

QY 82 KLENHNIGGYCFSMVL D-EPPKSLWMYSIPLNKLIRMNKAFNVVDVQFKSMPIQPLNLR 140

Db 74 -----gpfnfsvlispneqspweyseklkifiginvkfpavfsvqnpqulplyir 126

QY 141 VFLCFS-----NDVSAPVVRCQNHLSVEPLTANNAKMR---ESLLRSENPNSVYCGNAQ 191

Db 127 atpvisqtqhfdi---vhrvcvghr--hpqdgskngvaphifghlirctndnalyfgd-- 179

QY 192 GKGISERFSVWVPL---NMSRSVTRSGLTRQTLAFKFCVQNSC---IGRKETSLVFCLEK 245

Db 180 -kntgtlrnlvlpahpqvgedvvke-----ffqfvcnkscplgmrrridvvtled 231

QY 246 ACGDIVGQHVHVKICTCPKRDRIQDERQLNSKKRKSVPPEAAEEDPSKVRRCIAIKTED 305

Db 232 nkgevfgrrlvgvrvcscpkrdkdeekdmes-----avp-----prkrkrkl----- 274

QY 306 TESNDSRDCDDSAAEWNVSRTPDGD-----YRLAITCPNKEWLLQSIIEGMKEAAAEVLR 360

Db 275 --gnderrv-----vpqgssdnkifalnhihipgknylqalkmcqdm laneilk 321

QY 361 NPNQ 364

Db 322 kqeq 325

RESULT 4

AAAY50999

ID AAAY50999 standard; Protein; 636 AA.

XX

AC AAAY50999;

XX

DT 14-MAR-2000 (first entry)

XX

DE Human p73 protein.

XX

KW KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;

KW p53 family; angiogenic; cytotoxic; cancer; human; p73.

OS Homo sapiens.

XX

PN WO9961610-A2.

XX

PD 02-DEC-1999.

XX

PF 25-MAY-1999; 99WO-DE01557.

XX

PR 25-MAY-1998; 98DE-1022985.

XX

PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX

PI Paul D, Augustin M, Schmale H, Bamberger C;

XX

DR WPI; 2000-062710/05.

XX

PT New KET-encoding nucleic acid and related proteins, for diagnosis and

PT treatment of tumors -

XX

PS Disclosure; Fig 1; 28pp; German.

XX This invention describes a novel KET-encoding nucleic acid (I) and its

CC fragments, variants and mutants which has anticancer activity. (I)

CC encodes a protein, (II), involved in control of the cell cycle and

CC apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the

CC p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to

CC detect (I) in biological samples, specifically angiogenic tumor tissue,

CC including (I) sequences that have a homozygotic deletion and (b) to

CC detect presence or absence of human chromosome 3q27 or murine chromosome

CC 16, or their fragments, by hybridization. Also, (I) is used as a tumor

CC suppressor, particularly in tumors where an alteration in the wild-type

XX El-Deiry WS;
XX WPI; 2000-136954/12.
DR N-PSDB; AAZ49690.
XX Novel methods using p73 to induce apoptosis in E6- expressing cells
PT used to treat Human papillomavirus induced cancers
XX Claim 12; Page 42-43; 45pp; English.
XX The present sequence is a human p73 beta protein, which is a splice
CC variant of p73. p73 is a homolog of p53 tumour suppressor, capable of
CC arresting the growth of E6 protein-expressing cells. It is not targeted
CC for degradation by E6 oncoprotein and has been found to be a potent
CC inhibitor of cancer colony growth and inducer of apoptosis. Apoptosis
CC can be induced in E6-expressing cells, by administering p73 protein or a
CC DNA construct encoding p73. It can be used to treat human papilloma
CC virus (HPV) infections, cancers of the uterine cervix, anogenital,
CC oesophageal squamous cell cancer, laryngeal papilloma, and
CC bronchiolo-alveolar, penile and bladder carcinoma.
XX Sequence 499 AA;
SQ
Query Match 9.5%; Score 191; DB 21; Length 499;
Best Local Similarity 23.9%; Pred. No. 3.7e-11;
Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;
QY 17 EDDSTEVDIKEDIPKTVESGSELTTEPMFLQGLNSGNLMQFSQQSVLREMLQ----- 71
Db 23 epdstyfdlpqssrgnnvvgtdssmdvfhllegmttsvmaqfnllsstmdqmsraasa 82
QY 72 -----DIQIQANTLPKLENNHIGGYCFSMVLDE---PPKSL 104
Db 83 spytpehaasvpthspyaqpsstfdtmspapvipsntdyp-gphhfevtfqqsstaksat 141
QY 105 WMYSIPLNKLKLYIRMNKAFFNDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCONHLS 161
Db 142 wtyspllklycqiak--tcpikikvstpppgtairampvykkaehvtdvdkrcpnhel 199
QY 162 VEPLTANNAKMRSELLRSENP-SVYCGNAQKGKISERFSVVVPLNMSRVSRTSLTRQT 220
Db 200 grdfnegqsapashlirvegnnlsqyvddp---vtgrqsvvpy---epqvgvteftt 251
QY 221 LAFKFVCQNSCIG---RKETSLVFLCCKACGDIVGQHVHVHVKICTCPKRDRIQDE----- 272
Db 252 ilynfmcnsscvggnrrpiliitilemrdgqvlgrrrsfegricacpgdrkadedhyre 311
QY 273 -RQLN--SKKRKSVPEAAEEDPSKV 295
Db 312 qqalnessakngaaskrafkqspav 337
RESULT 7
AAW30661
ID AAW30661 standard; Protein; 635 AA.
XX
AC AAW30661;
XX
DT 07-APR-1999 (first entry)
XX
DE Human NBS-1 alpha protein.
XX
KW Human; NBS-1; p73; antibody; p53 responsive element; p53 promoter;
KW p53-dependent tumour; growth inhibition.
XX
OS Homo sapiens.
XX
PN W09851350-A1.
XX
PD 19-NOV-1998.
XX

PF 12-MAY-1998; 98WO-US09516.
XX
PR 12-MAY-1997; 97US-0046207.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Jost C, Kaelin W;
XX
DR WPI; 1999-059690/05.
XX
PT Treating subjects using NBS-1 proteins and antibodies - used to
PT interact with p53-responsive genes and inhibit growth of
PT p53-dependent tumour cells
XX
PS Example; Fig 1A; 65pp; English.
XX
CC A method has been developed for treating a subject having a
CC p53-dependent tumour cell. The method comprises: (a) determining the
CC level of NBS-1 protein (also known as p73) expressed in the tumour
CC cell and in a corresponding non-malignant cell; (b) selecting subjects
CC having NBS-1 protein level comparable or below that in a corresponding
CC normal cell; (c) elevating tumour cell NBS-1 level, where NBS-1
CC interacts with p53-responsive promoters. Also described in the present
CC invention is an antibody that specifically binds to NBS-1, and an
CC antibody raised to the carboxy portion of NBS-1. NBS-1 can activate the
CC transcription of p53-responsive genes and can inhibit cell growth in a
CC p53-like manner. The present sequence represents the human NBS-1 alpha
CC protein from the present invention.
XX
SQ Sequence 635 AA;
Query Match 9.5%; Score 191; DB 20; Length 635;
Best Local Similarity 23.9%; Pred. No. 5.4e-11;
Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;
QY 17 EDDSTEVDIKEDIPKTVESGSELTTEPMFLQGLNSGNLMQFSQQSVLREMLQ----- 71
Db 23 epdstyfdlpqssrgnnvvgtdssmdvfhllegmttsvmaqfnllsstmdqmsraasa 82
QY 72 -----DIQIQANTLPKLENNHIGGYCFSMVLDE---PPKSL 104
Db 83 spytpehaasvpthspyaqpsstfdtmspapvipsntdyp-gphhfevtfqqsstaksat 141
QY 105 WMYSIPLNKLKLYIRMNKAFFNDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCONHLS 161
Db 142 wtyspllklycqiak--tcpikikvstpppgtairampvykkaehvtdvdkrcpnhel 199
QY 162 VEPLTANNAKMRSELLRSENP-SVYCGNAQKGKISERFSVVVPLNMSRVSRTSLTRQT 220
Db 200 grdfnegqsapashlirvegnnlsqyvddp---vtgrqsvvpy---epqvgvteftt 251
QY 221 LAFKFVCQNSCIG---RKETSLVFLCCKACGDIVGQHVHVHVKICTCPKRDRIQDE----- 272
Db 252 ilynfmcnsscvggnrrpiliitilemrdgqvlgrrrsfegricacpgdrkadedhyre 311
QY 273 -RQLN--SKKRKSVPEAAEEDPSKV 295
Db 312 qqalnessakngaaskrafkqspav 337
RESULT 8
AAW36184
ID AAW36184 standard; Protein; 636 AA.
XX
AC AAW36184;
XX
DT 27-APR-1998 (first entry)
XX
DE Human p53 tumour suppressor-related protein SR-p70a.
XX
KW SR-p70; human; transcription factor; p53; tumour suppressor gene;
KW homology; differential splicing; diagnosis; cancer; neuroblastoma;

KW gene therapy; apoptosis.
XX Homo sapiens.
OS WO9728186-A1.
XX 07-AUG-1997.
PD XX 03-FEB-1997; 97WO-FR00214.
XX 02-FEB-1996; 96FR-0001309.
PR XX (SNFI) SANOFI SA.
XX Caput D, Ferrara P, Kaghad AM;
PI WPI; 1997-402550/37.
XX N-PSDB; AAV01498.
DR XX New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
PT and related nucleic acid, useful for diagnosis and treatment of
PT tumours
XX Claim 7; Fig 6; 136pp; French.
PS This is the amino acid sequence of the human protein SR-p70a. SR-p70
XX are transcription factors which may control the activity of
CC p53-regulated genes, and are expressed by tumour suppressor genes related
CC to the p53 gene family. The gene sequence was isolated from the human
CC colon adenocarcinoma cell line HT-29, using primers AAV01506-7. The
CC sequence can be used in the diagnosis and monitoring of cancer,
CC especially neuroblastoma. The nucleic acid sequences and corresponding
CC antisense sequences, are also useful in gene therapy, e.g. to regulate
CC apoptosis.
XX Sequence 636 AA;
SQ
Query Match 9.5%; Score 191; DB 18; Length 636;
Best Local Similarity 23.9%; Pred. No. 5.5e-11;
Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;
QY 17 EDDSTEVDIKEDIPKIVEVSGSELTEPMAFLQGLNSGNLMQFSQQSVLRMMLO----- 71
Db 23 epdstyfdlpqssrgnnevvgtdssmdvfhlegmttsvmaqfnllsstmdqmsraasa 82
QY 72 -----DIQIQANTLPKLENHNIGGCFSMVLDE---PPKSL 104
Db 83 spytpehaasvpthspyaqpsstfdtmspavipsntdyp-gphhfevtfggstaksat 141
QY 105 WMYSIPLNKLKLYIRMNKAFAFNDVQFKSKMPIQP-LNLRVFLCF--SNDVSAFVVRQCNHLS 161
Db 142 wtyspllklycqiak--tcpiqikvstpppgptairampvykkaehvtdvkrpcpnhel 199
QY 162 VEPLTANNAKMRESLLRSENPN-SVYCGNAQKGKISERFSVVVPLNMSRSVTRSGLTRQT 220
Db 200 grdfneggsapashlirvegnnlsqyvddp-----vtgrqsvvpy---epqvgteftt 251
QY 221 LAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIQDE----- 272
Db 252 ilynfmcnsscvgmrrpiliitilemrdgqvlgrrsfegricacpgrdrkadedhyre 311
QY 273 -RQLN--SKKRKSVPEAAEEDEPSKV 295
Db 312 qqalnessakngaaskrafkqspav 337
RESULT 9
AA44634
ID AAY44634 standard; Protein; 636 AA.
XX
AC AAY44634;
XX

DT 07-APR-2000 (first entry)
XX Human p73 alpha splice variant protein.
DE XX
XX p73; splice variant; human; p73 alpha; p53 tumour suppressor;
KW E6; oncoprotein; inhibitor; apoptosis; human papilloma virus; HPV;
KW cancer; uterine cervix; anogenital; oesophageal squamous cell;
KW laryngeal papilloma; bronchiolo-alveolar; penile; bladder; carcinoma.
XX Homo sapiens.
OS WO9966946-A1.
XX 29-DEC-1999.
PN 23-JUN-1999; 99WO-US14057.
XX 24-JUN-1998; 98US-0090526.
PR (UYPE-) UNIV PENNSYLVANIA.
XX El-Deiry WS;
PI WPI; 2000-136954/12.
DR N-PSDB; AAZ49690.
DR Novel methods using p73 to induce apoptosis in E6- expressing cells
XX used to treat Human papillomavirus induced cancers -
XX Claim 12; Page 40-41; 45pp; English.
PS The present sequence is a human p73 alpha protein, which is a splice
XX variant of p73. p73 is a homolog of p53 tumour suppressor, capable of
CC arresting the growth of E6 protein-expressing cells. It is not targeted
CC for degradation by E6 oncoprotein and has been found to be a potent
CC inhibitor of cancer colony growth and inducer of apoptosis. Apoptosis
CC can be induced in E6-expressing cells, by administering p73 protein or a
CC DNA construct encoding p73. It can be used to treat human papilloma
CC virus (HPV) infections, cancers of the uterine cervix, anogenital,
CC oesophageal squamous cell cancer, laryngeal papilloma, and
CC bronchiolo-alveolar, penile and bladder carcinoma.
XX Sequence 636 AA;
SQ
Query Match 9.5%; Score 191; DB 21; Length 636;
Best Local Similarity 23.9%; Pred. No. 5.5e-11;
Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;
QY 17 EDDSTEVDIKEDIPKIVEVSGSELTEPMAFLQGLNSGNLMQFSQQSVLRMMLO----- 71
Db 23 epdstyfdlpqssrgnnevvgtdssmdvfhlegmttsvmaqfnllsstmdqmsraasa 82
QY 72 -----DIQIQANTLPKLENHNIGGCFSMVLDE---PPKSL 104
Db 83 spytpehaasvpthspyaqpsstfdtmspavipsntdyp-gphhfevtfggstaksat 141
QY 105 WMYSIPLNKLKLYIRMNKAFAFNDVQFKSKMPIQP-LNLRVFLCF--SNDVSAFVVRQCNHLS 161
Db 142 wtyspllklycqiak--tcpiqikvstpppgptairampvykkaehvtdvkrpcpnhel 199
QY 162 VEPLTANNAKMRESLLRSENPN-SVYCGNAQKGKISERFSVVVPLNMSRSVTRSGLTRQT 220
Db 200 grdfneggsapashlirvegnnlsqyvddp-----vtgrqsvvpy---epqvgteftt 251
QY 221 LAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIQDE----- 272
Db 252 ilynfmcnsscvgmrrpiliitilemrdgqvlgrrsfegricacpgrdrkadedhyre 311
QY 273 -RQLN--SKKRKSVPEAAEEDEPSKV 295
Db 312 qqalnessakngaaskrafkqspav 337

Db 83 spytpehaasvthspyaqpsstfdtmspapvipsntdyp-gphhfevtfqsstaksat 141
QY 105 WMYSIPLNKLIRMNKAFNVDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCONHLS 161
Db 142 wtyspllklyqiaak--tcpikvksapppgtairampvykkaehvtdivkrcpuhel 199
QY 162 VEPLTANNAKMRSELLRSENPN-SVYCGNACGKGISERFSVWVPLNMSRSVTRSGLTRQT 220
Db 200 grdfnegqsapashlirvegnlsqyvddp---vtgrqsvvpy----epqvgteftt 251
QY 221 LAFKFVCQNSCIG--RKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIQDE----- 272
Db 252 ilynfmcnsscvggmrrpiliitltetrdgqvlgrrrsfegricacpgrdrkadedhyre 311
QY 273 -RQLN--SKKRSKVPEAAEEDPSKV 295
Db 312 qqalnessakngaaskrafkgsppav 337

RESULT 12
AAY45246
ID AAY45246 standard; Protein; 448 AA.
XX
AC AAY45246;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human p51 protein A.
XX
KW Human; p51; p53 related gene; cell proliferation; regulation; cancer;
KW tumour suppression; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..59
FT /label= transactivation_domain
FT 142..321
FT /label= DNA_binding_domain
FT 353..397
FT /label= oligomerisation_domain
XX
PN WO9950412-A1.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-JP01512.
XX
PR 27-MAR-1998; 98JP-0100467.
XX
PA (SAKA) OTSUKA PHARM CO LTD.
PA (IKAW/) IKAWA Y.
XX
PI Ikawa Y, Ikawa S, Obinata M;
XX
DR WPI; 1999-591318/50.
DR N-PSDB; AAZ25770.
XX
PT New p53 related human gene p51, useful for diagnosis, investigation and
PT treatment of cancers and screening for potential cell proliferation
PT agents -
XX
PS Claim 1; Page 147-148; 163pp; Japanese.
XX

CC The present sequence represents a human p51 protein, which is related to
CC p53 and has cell proliferation regulation and tumour suppression
CC activity. The p51 gene can be used in the investigation, diagnosis and
CC treatment of diseases such as cancer, with which the p53 family cell
CC proliferation regulation is associated. The p51 protein may be used for
CC screening potential agonists and antagonists of its regulatory function,
CC for use as drugs,
XX
SQ Sequence 448 AA;

Query Match 9.3%; Score 186; DB 20; Length 448;
Best Local Similarity 22.2%; Pred. No. 1e-10;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;
QY 5 QPMSWHKESDSEDST-EVDIKEDIPKTEVSVSGSELTEPMAFLQGLNSGNLMQFSQQS 63
Db 31 qpdlinfvdepsedgatnkiesmd---cirmqdsdl-sdpm-----wpqytnlg 76
QY 64 VLREMLLDIQIQ---ANTLPKLENH-----NI 88
Db 77 llmsm---dqiqngssstpyntdhagnsvtapsyaqpsstfdalspsaipstndyp 133
QY 89 GGYCFSMVLDE---PPKSLWMYSIPLNKLIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF 145
Db 134 gphsfvsgsstaksatwtystelkklycqiaktcpikvmtppp-qgavirampvy 192
QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRSELLRSENPNVYCGNACGKGISE-----RF 199
Db 193 kkaehvtevkrpcnhelsrefnegqiappshlirve-----gnshaqyvedpitgrq 245
QY 200 SVVVPILNMSRSVTRSGLTRQTLAFKFVCQNSCIG--RKETSLVFCLEKACGDIVGQHV 256
Db 246 sylvpy---epqvgteftvlynfmcnsscvggmrrpiliitltetrdgqvlgrref 301
QY 257 HVKICTCPKRDRIQDERQLNSKKRSKVPEAAEEDPSK 294
Db 302 earicacpgrdrkade---dsirkqvsdstkngdgtk 336

RESULT 13
AAY05955
ID AAY05955 standard; Protein; 448 AA.
XX
AC AAY05955;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cell regulatory protein p63, isoform huTap63 gamma.
XX
KW Cell regulatory protein; p63; huTap63 gamma; Tap63 gamma; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.
XX
OS Homo sapiens.
XX
PN WO9919357-A2.
XX
PD 22-APR-1999.
XX
PF 02-OCT-1998; 98WO-US21992.
XX
PR 29-MAY-1998; 98US-0087216.
PR 15-OCT-1997; 97US-0062076.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI McKeon F, Yang A;
XX
DR WPI; 1999-277595/23.
DR N-PSDB; AAX58574.
XX
PT New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
XX
PS Claim 23; Fig 11; 161pp; English.
XX
CC The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from

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OM protein - protein search, using sw model

Run on: November 16, 2001, 15:05:43 ; Search time 31.25 Seconds
(without alignments)
277.241 Million cell updates/sec

Title: US-09-524-101-2
Perfect score: 2008
Sequence: 1 WYISQPM5WHKESTDSEDDS.....NLRHANKLLSLKKRAYELP 385

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183.5	9.1	381	4	US-09-257-580-2 Sequence 2, Appli
2	167.5	8.3	390	1	US-08-347-792-15 Sequence 15, Appl
3	167.5	8.3	390	1	US-08-431-357-15 Sequence 15, Appl
4	167.5	8.3	390	4	US-08-392-542-3 Sequence 3, Appli
5	167.5	8.3	390	4	US-08-894-327-3 Sequence 3, Appli
6	167.5	8.3	390	5	PCT-US95-15353-15 Sequence 15, Appl
7	162	8.1	393	2	US-08-697-221-3 Sequence 3, Appli
8	162	8.1	393	2	US-08-697-221-4 Sequence 4, Appli
9	160	8.0	363	2	US-08-697-221-18 Sequence 18, Appl
10	160	8.0	393	1	US-08-047-041A-25 Sequence 25, Appl
11	160	8.0	393	1	US-08-047-041A-26 Sequence 26, Appl
12	160	8.0	393	1	US-08-047-041A-27 Sequence 27, Appl
13	160	8.0	393	1	US-08-047-041A-28 Sequence 28, Appl
14	160	8.0	393	1	US-08-347-792-2 Sequence 2, Appli
15	160	8.0	393	1	US-08-390-516C-6 Sequence 6, Appli
16	160	8.0	393	1	US-08-390-516C-7 Sequence 7, Appli
17	160	8.0	393	1	US-08-390-516C-8 Sequence 8, Appli
18	160	8.0	393	1	US-08-390-516C-9 Sequence 9, Appli
19	160	8.0	393	1	US-08-431-357-2 Sequence 2, Appli
20	160	8.0	393	1	US-08-390-515A-6 Sequence 6, Appli
21	160	8.0	393	1	US-08-390-515A-7 Sequence 7, Appli
22	160	8.0	393	1	US-08-390-515A-8 Sequence 8, Appli
23	160	8.0	393	1	US-08-390-515A-9 Sequence 9, Appli
24	160	8.0	393	2	US-08-795-006A-32 Sequence 32, Appl
25	160	8.0	393	2	US-08-697-221-2 Sequence 2, Appli
26	160	8.0	393	2	US-08-801-718-6 Sequence 6, Appli
27	160	8.0	393	2	US-08-801-718-7 Sequence 7, Appli

28	160	8.0	393	2	US-08-801-718-8 Sequence 8, Appli
29	160	8.0	393	2	US-08-801-718-9 Sequence 9, Appli
30	160	8.0	393	2	US-08-247-904B-12 Sequence 12, Appl
31	160	8.0	393	2	US-08-675-631-1 Sequence 1, Appli
32	160	8.0	393	3	US-08-767-942A-23 Sequence 23, Appl
33	160	8.0	393	4	US-08-392-542-2 Sequence 2, Appli
34	160	8.0	393	4	US-09-184-073-32 Sequence 32, Appl
35	160	8.0	393	4	US-08-328-673A-9 Sequence 9, Appli
36	160	8.0	393	4	US-08-894-327-2 Sequence 2, Appli
37	160	8.0	393	5	PCT-US95-15353-2 Sequence 2, Appli
38	160	8.0	439	2	US-08-959-638-9 Sequence 9, Appli
39	159	7.9	393	2	US-08-697-221-15 Sequence 15, Appl
40	158	7.9	363	2	US-08-697-221-17 Sequence 17, Appl
41	158	7.9	393	2	US-08-697-221-14 Sequence 14, Appl
42	158	7.9	393	2	US-08-697-221-27 Sequence 27, Appl
43	157	7.8	363	2	US-08-697-221-22 Sequence 22, Appl
44	157	7.8	393	2	US-08-697-221-12 Sequence 12, Appl
45	157	7.8	393	2	US-08-697-221-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-257-580-2
; Sequence 2, Application US/09257580
; Patent No. 6307036
; GENERAL INFORMATION:
; APPLICANT: Yorkshire Cancer Research
; TITLE OF INVENTION: Tumour Suppressor Gene
; FILE REFERENCE: Canine p53
; CURRENT APPLICATION NUMBER: US/09/257,580
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 9804178.3
; PRIOR FILING DATE: 1998-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Canis
US-09-257-580-2

Query Match	9.1%	Score 183.5;	DB 4;	Length 381;
Best Local Similarity	23.3%	Pred. No. 2.4e-11;		
Matches	66;	Conservative 45;	Mismatches 109;	Indels 63; Gaps 11;
QY	105	WMYSIPLNKLYIRMNKAFFNVQVQFKSMPIQPLNLRVLCF--SNDVSAPVVRCONHLSV	162	
Db	111	WTYSPLLNKLFQOLAKTCVPQLWVSSPPPTNC-VRAMAIYKKSEFTEVVRRCPPHERC	169	
QY	163	EPLTANNAKMRESLLRSENPNVYCGNAGQKGISE----RFSVVVPLNMSRSVTRSGLTR	218	
Db	170	SD-SSDGLAPPQHLIRVE-----GNLRKAYLDDRNTRHSHVVVPY----EPPEVGSDY	217	
QY	219	QTLAFKFVCONSCIG---RKETSLVFCLEKACGDIVGQVHIVHKICTCPKRDRIQDERQL	275	
Db	218	TTIHYNMCMSSCMGMNRRPILTIITLEDSSGNVLGRNSFEVRVCACPGDRDRTEENF	277	
QY	276	NSKKRKSVPEAAEEDPSKVRRCIAIKTEDTESNDRDCDDSAAEWNVSRTPDGYRLAI	335	
Db	278	HKK-----GEPCEPPPGSTKRALPPSTSSSPQKKKPL-----DGEY----	315	
QY	336	TCPNKEWLLQSIEMIKAAAAEVLNPNQENLRRHANKLLSLK	378	
Db	316	-----FTLQ-----IRGRERYEMFRNLNEALELK	339	

RESULT 2
US-08-347-792-15
; Sequence 15, Application US/08347792
; Patent No. 5573925

GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
Tetramerization Domains
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,792
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST58USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-347-792-15

Query Match 8.3%; Score 167.5; DB 1; Length 390;
Best Local Similarity 25.6%; Pred. No. 1.3e-09;
Matches 60; Conservative 38; Mismatches 95; Indels 41; Gaps 10;
QY 107 YSIPLNKLKLYIRMNKAFFNDVQFKSKMPIOPLNLRVFLCF--SNDVSAVVVRQNHLSVPE 164
Db 123 YSPPLNKLKFCQLVKTCVQL-WVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPPHERCS- 180
QY 165 LTANNAKMRESLLRSENPNVYCGNAQKGISE----RFSVVVPLNMSRVSFTSGLTRQT 220
Db 181 -DGDGLAPPQHLIRVE-----GNLYPEYLEDRTQFRHSVVVPPY----EPPEAGSEYTT 228
QY 221 LAFKFCVQNSCIG---RKETSLVFCLEKACGDIYQHVHVKICTCPKRDRIQDERQLNS 277
Db 229 IHKYMNCSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRCACPGDRDRTEENFR- 287
QY 278 KKRKSVPAAEEDEPSKVRRCIAIKTEDTESNLRDCCDDSAAEWNVSRTPDGDY 331
Db 288 KKEVLCPDEL---PPGSAKRALPTCT-----SASPPQKKKPLDGEY 324

RESULT 3
US-08-431-357-15
Sequence 15, Application US/08431357
Patent No. 5721340
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
Tetramerization Domains
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA

ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST58USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-431-357-15
Query Match 8.3%; Score 167.5; DB 1; Length 390;
Best Local Similarity 25.6%; Pred. No. 1.3e-09;
Matches 60; Conservative 38; Mismatches 95; Indels 41; Gaps 10;
QY 107 YSIPLNKLKLYIRMNKAFFNDVQFKSKMPIOPLNLRVFLCF--SNDVSAVVVRQNHLSVPE 164
Db 123 YSPPLNKLKFCQLVKTCVQL-WVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPPHERCS- 180
QY 165 LTANNAKMRESLLRSENPNVYCGNAQKGISE----RFSVVVPLNMSRVSFTSGLTRQT 220
Db 181 -DGDGLAPPQHLIRVE-----GNLYPEYLEDRTQFRHSVVVPPY----EPPEAGSEYTT 228
QY 221 LAFKFCVQNSCIG---RKETSLVFCLEKACGDIYQHVHVKICTCPKRDRIQDERQLNS 277
Db 229 IHKYMNCSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRCACPGDRDRTEENFR- 287
QY 278 KKRKSVPAAEEDEPSKVRRCIAIKTEDTESNLRDCCDDSAAEWNVSRTPDGDY 331
Db 288 KKEVLCPDEL---PPGSAKRALPTCT-----SASPPQKKKPLDGEY 324

RESULT 4
US-08-392-542-3
Sequence 3, Application US/08392542
Patent No. 6169073
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
APPLICANT: Hartwig, Wolfgang
TITLE OF INVENTION: Peptides nad Peptidomimetics with
Structural Similarity to Human p53 That Activate p53
TITLE OF INVENTION: Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

QY	107	YSIPLNKLIRMNKAFNDVDVQFKSKMPIQLNLRVFLCF--SNDVSAPVRQCQNHLSVEP	164
Dd	123	YSPPLNKLFCQLVKTCPVQL-WVSATPPAGSRVRAMAIYKKSHMTVVRRCPHHERCS-	180
QY	165	LTANNAKMRESLLRSENPNSVYCNGAOGKGISE---RFSVVVPLNMRSVTRSGLTRQT	220
Dd	181	-DGDGLAPPQHILRVE-----GNLYPEYLEDROGTFHRHSVVVPY---EPPEAGSEYTT	228
QY	221	LAFKFVCONSCIG--RKETSLVFCKLEKACGDIVCQHVHVXIKCTCPKRBDIQDERQLNS	277
Dd	229	IHYKYMNCSSCMGMNRRLPTITILEDSSGNLGRDSFEV VCACPGRDRRTTEENFR-	287
QY	278	KRRKSVPAAEEDEPSKVRCIAIKTEDTESNDSRDCDDSAWNVVSRTPDGDY	331
Dd	288	KKEVLCPHEL----PPGSAKRALPTCT-----SASPOKKKKPLPDGEY	324

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RESULT 7
US-08-697-221-3
; Sequence 3, Application US/08697221
; Patent No. 5847083
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: Modified p53 Constructs and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/697,221
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,802
; FILING DATE: 22-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST64AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-697-221-3

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Query Match      8.1%; Score 162; DB 2; Length 393;
Best Local Similarity 23.0%; Pred. No. 5.3e-09;
Matches 65; Conservative 52; Mismatches 121; Indels 44; Gaps 11;

QY 107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQLNLRVFLCF--SNDVSAPVVVRCONHLSVEP 164
      || |||::: || |:: | | | | | | | | | | | | | | | | | | | | | | | |
Db 126 YSPALNMFCQLAKTCPVQLWDSTPP-PGTRVRAMAIYKQSQHMTVEVRRCPHERCS- 183
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 165 LTANNAKMRESLLRSENPNSVYCGNAQKGISE---RFSVVVPLNMRSRVTBSGLTRQT 220
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Db 184 -DSDGLAPPQHLIRVE-----GNLRVEYLDORNTFRHSVVVPY---EPPEVGSDCCT 233
QY 221 LAFKFVCQNSCIG--RKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIQDERQLNS 277
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 IHNYMCNSSCMGMMRRPILTIITLEDSSGNLLGRNSFEVRCACACGRRDRREENLRK 291
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 278 KKRKSVPAAEEDEPSKVPRCIAKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAIT 336
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 K-----GEPHELPPGSKRALPNNT-----SSSPQPKKKPLDGEYFTLQIR 333
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 CPNKEWLLQSIEGMIKEAAAEVLNPNQENLRHRHANKLLSLK 378
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 334 GRERFEMFREINAELEKDAQAGKEG--GSRHSSHLSKSK 373
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-08-697-221-4
; Sequence 4, Application US/08697221
; Patent No. 5847083
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: Modified p53 Constructs and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: i:ntentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/697,221
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,802
; FILING DATE: 22-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST64AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-697-221-4

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	Query Match	8.1%;	Score 162;	DB 2;	Length 393;	
	Best Local Similarity	23.0%;	Pred. NO. 5.3e-09;			
Matches	65;	Conservative	52;	Mismatches 121;	Indels 44;	Gaps 11;
QY	107	YSTPLNKLYIRMNKAFNVDVQFSKMPIQPLNLRVLCF--	SNDVSA	PVVR	CQNHLSVEP	164
		:: :: : : : : : :				
Db	126	YSPALNMFCQLAKTCPVQLWVDSTPP-PGTRVRAMAIYKQSQHMT	EVVRR	CPHHERCS-	183	
QY	165	LTANNAKMRESLLRSENPNSVYCNAQKGISE----	RFSVVV	PLNM	SRSVTRSGLTRQT	220
		:: : : : : : : : : :				
Db	184	-DSDGLAPPQHLIRVE-----GNLRVEYLDORNTFRHSVVVPY----	EPPEV	SGDCTT	231	
QY	221	LAFKEVQNSCIG---RKETSLVFCLEKACGDIVGQHVHVIKICTCPKRDRIO	DFQLNS	277		

Db 232 IHNYMCMSSCGMNRRLPILTIITLEDSSGNLLGRNSFEVRVCACPGDRDRRKEENLRK 291
QY 278 KKRKSVPEAAEEDPSKVRRCIAIKTEDTESNDRDCDDSAAEWNVSRTPDGDYRLAITC 337
Db 292 K-----GEPHELPPGSTYKRALPNNT-----SSSPQPKKKPLDGEY----- 327
QY 337 CPNKEWLLQSIGMIKEAAAEVLNPNQENLRRHANKLLSLK 378
Db 334 GRERFEMFRELNEALELKAQAGKEPG--GSRHSSHLKSKK 373

RESULT 9
US-08-697-221-18
; Sequence 18, Application US/08697221
; Patent No. 5847083
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: Modified p53 Constructs and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/697,221
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,802
; FILING DATE: 22-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST64AUSA
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-697-221-18

Query Match 8.0%; Score 160; DB 2; Length 363;
Best Local Similarity 22.8%; Pred. No. 7.7e-09;
Matches 64; Conservative 47; Mismatches 106; Indels 64; Gaps 11;

QY 107 YSIPLNKLIRMNKAFNVQFKSKMPIQLNLRVFLCF--SNDVSAPVVRCONHLSVEP 164
Db 126 YSPALNKMFCQLAKTCVQLWVDSTPP-PGTRVRMAIYKQSQHMTVEVRRCPHERCS- 183
QY 165 LTANNAKMRESLLRSENPNVYCGNAGKGISE----RFSVVVPLNMSRVSRTSGLTRQT 220
Db 184 -DSDGLAPQHLIRVE-----GNLVEYLDNRFRHSVVVPY----EPPEVGSDCIT 231
QY 221 LAFKFCVQNSCIG---RKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIQDERQLNS 277
Db 232 IHNYMCMSSCGMNRRLPILTIITLEDSSGNLLGRNSFEVRVCACPGDRDRRKEENLRK 291

QY 278 KKRKSVPEAAEEDPSKVRRCIAIKTEDTESNDRDCDDSAAEWNVSRTPDGDYRLAITC 337
Db 292 K-----GEPHELPPGSTYKRALPNNT-----SSSPQPKKKPLDGEY----- 327
QY 338 PNKEWLLQSIGMIKEAAAEVLNPNQENLRRHANKLLSLK 378
Db 328 -----FTLQ-----IRGRERFEMFRELNEALELK 351
RESULT 10
US-08-047-041A-25
; Sequence 25, Application US/08047041A
; Patent No. 5527676
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Baker, Suzanne J.
; APPLICANT: Fearon, Eric R.
; APPLICANT: Nigro, Janice M.
; TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/047,041A
; FILING DATE: 22-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/928,661
; FILING DATE: 17-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/446,584
; FILING DATE: 06-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/330,566
; FILING DATE: 29-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42917
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Buchman, et al.,
; JOURNAL: Gene
; VOLUME: 70
; PAGES: 245-252
; DATE: 1988
; US-08-047-041A-25

Query Match 8.0%; Score 160; DB 1; Length 393;


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Best Local Similarity 23.0%; Pred. No. 8.8e-09;
Matches 65; Conservative 51; Mismatches 122; Indels 44; Gaps 11;

QY 107 YSIPLNKLYIRMNKAENVVDYQFKSKMPIQLPLNLRVFLCF--SNDVSAPVVRCONHLSVEP 164
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Db 126 YSPALNKMFCQLAKTCPVOLWVDSTPP-PGTRVFAVAIYKQSQHMTVEVRRCPHERCS- 183
   || |||:: :: | | : | | : | | : | | : | | : | | : | | : | | : |
QY 165 LTANNAKMRESLLRSENPNNSVYCGNAQCKGISE----RFSVVVPLNMRSVTRSGLTROT 220
   :: | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 184 -DSDGLAPPQHLIRVE-----GNLRVEYLLDRNTRFHSVVVPY----EPPEVGSDDTT 231
   :: | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 221 LAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIVHKICTCPKRDRIQDERQLNS 277
   : : | | : || | | | : : | | : |||:: : | | : |||:: : | | : | | : |
Db 232 IHNYMCNSSCMGMNRRPILTTITLEDSSGNLLGRNSFEVRVCACPGDRDRTEENLRK 291
   : : | | : || | | | | | | | | | | | | | | | | | | | | | | | | |
QY 278 KKRKSVPAAEEDPSKVRRCIAIKTEDTESNDSRDCDDSAEENNVSRTPDGDY-RLAIT 336
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 292 K-----GEPHHELPPGSTKRALPNNT-----SSSQPKKKPLDGEYFTLQIR 333
   : : | | : || | | | | | | | | | | | | | | | | | | | | | | | | |
QY 337 CPNKEWLLQSIEMIKAEAAEVLNPNQENLRRHANKLLSLK 378
   : : : : : : : : | | : | | : | | : | | : | | : | | : | | : |
Db 334 GRERFEMFREINALELKDAQAGKEPG--GSRHSHSLKSKK 373
   : : | | : || | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-08-047-041A-26
; Sequence 26, Application US/08047041A
; Patent No. 5527676
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Baker, Suzanne J.
; APPLICANT: Fearon, Eric R.
; APPLICANT: Nigro, Janice M.
; TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001.4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/047,041A
; FILING DATE: 22-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/928,661
; FILING DATE: 17-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/446,584
; FILING DATE: 06-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/330,566
; FILING DATE: 29-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42917
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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RESULT 15
US-08-390-516C-6
; Sequence 6, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.

QY	107	YSIPLNKLYIRMNKAENVDVQFKSKMPEIQPLNLRVFLCF--SNDVSAPVVRCONHLSVEP	164
Dd	126	YSPALNMFCQLAKTCPQLWVDSTPP-PGTRVRAMAIYKQSQHMTFVRRCPHERCS-183	
QY	165	LTANNAKMRESLLRSENPNFSVYCNGAOGKGISE---RFSVVVPLNMSRSVTRSGLTROT	220
Dd	184	-DSDGLAPPQHLIRVE-----GNLRVEYLDDRNTRHSVVVPY----EPPEVGSDCTT	231
QY	221	LAFKFVCQNSCIG--RKETSLVFCLKACGDIVCGQHVHVKICTCPKRDRIDQDERQLNS	277
Dd	232	IHYNYMCNSSCMGMNRPIILTITLEDSSGNLLGRNSFEVRCACPGDRDRTEENLRK	291
QY	278	KRKSVPERAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAIT	336
Dd	292	K-----GEPHHELPPGSTKRALPNNT-----SSSQPKKKPLDGeyFTLQIR	333
QY	337	CPNKEWLLQSIEGMKBAAAEVLNPQNLENRRHANKLLSLK	378
Dd	334	GREFEFMEFRELNEALETKDAQAGKEPG--GSRAHSSHLLKSCK	373

Search completed: November 16, 2001, 15:49:51
Job time: 2648 sec

A;Reference number: S72313
A;Accession: S72313
A;Molecule type: mRNA
A;Residues: 1-51,'S',53-70,72-293,295-363 <HOW>
A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
C;Genetics:
A;Gene: p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F;150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

	Query Match	8.8%;	Score 176.5;	DB 1;	Length 363;
	Best Local Similarity	26.2%;	Pred. No. 7e-07;		
	Matches	73;	Conservative 46;	Mismatches 119;	Indels 41; Gaps 13;

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QY      55 NLMQFSQQSVLRMMMLQDIQIQTANTLPKLEHNHI-----GGYCFSMVLDE--PPKSL- 104
       ||:||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db      38 NLSEFPDYPLAADMTVLOEGLMGNAVPTVTSCAVPSTDYAGKYGLQLDFQQNGTAKSVT  97

QY     105 WMYSIPLNKLYIRMKAFNVVDVFQFKSKMPIQPLNLRVFLCF--SNDVSAPVVRCQNHL-LS 161
       ||||||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: |
Db      98 CTYSPELNKLFQLAKTCTPLLVRVESPPPRGSI-LRATAVKKSEHVAEVVKRGPHHERS 156

QY     162 VEPLTANNAKMRRESLLRSENPNNSVYCNAQGKGI----SERFSVVVPLNMRSRSTRSGLT 217
       ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|
Db     157 VEP--GEDAAPPSHLMRVE-----GNLQAYMEDVNSGRHSVCVPY---EGPQVGTE 203

QY     218 RQTIAKFVCONSCIG---RKETSLVFCLEKACGDIVGQHVIHVXICTCPKRDRIQDERQ 274
       ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|
Db     204 CTTVLYNYMCSSCMGMNRRLPILTIITLETPOGLLGRRRCFEVRVCACPGRDR-RTEED 262

QY     275 LNSKKRKSVPEAAEE-----DEPSKVRRCIAIKTETE 307
       :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     263 NYTKKRGPKSGKRELAHPSPSEPPLPKKRLVVVDDEE 301

RESULT    4
JH0633
cellular tumor antigen p53 - golden hamster
N:Alternate names: tumor-suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0633
R:Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A>Title: The cDNA cloning and immunological characterization of hamster p53.
A;Reference number: JH0633; MUID:92210007
A;Accession: JH0633
A;Molecule type: mRNA
A;Residues: 1-396 <LEG>
A;Cross-references: GB:M75144; NID:g191414; PIDN:AAA37085.1; PID:g191415
A;Experimental source: kidney, strain MP1
C;Genetics:
A;Gene: p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F;179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
```

	Query Match	8.7%;	Score 174;	DB 1;	Length 396;
	Best Local Similarity	24.9%;	Pred. No. 1.3e-06;		
	Matches	70;	Conservative 51;	Mismatches 118;	Indels 42; Gaps 12;

```

QY     107 YSIPLNKLYIRMKAFNVVDVFQFKSRMP-----IQPLNLRVFLCFSDVSAPIVVRQNHLSV 162
       ||||||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: |
Db     129 YSPSLNKLFCQLAKTCVQLWSSPPPGTRVRAMAIYKKLOYMTEV---VRRCPHH--E 183

QY     163 EPLTANNAKMRRESLLRSE-NPNSVYCNAQGKISERFSVVVPLNMRSRSTRSGLTROTFL 221
       :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db     184 RSSEGDCGLAPPQHLIRVEGNMHAELDDKQ-----TFRHSSVVVPY----EPPEVGSDCCTTII 2235
```

QY	222	AFKFVCQN	SICG--RKETSLVFCLEKACGDIVGOHVHVKICTCPKRDRIODERQLNSK	278
		:	: : : : :	
		:	: : : : :	
DB	236	HNYMCNSSCGMNRRLPILTIITLEDPSGNLLGRNFEVRICACPGDRDRTEKNF-QK	294	
		:	: : : : :	
		:	: : : : :	
QY	279	KRKSVPAAAEDEPSKVRRRCIAKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAIRC	337	
		:	: :	
		:	: :	
DB	295	KGEPCPEL----PPKSARALPTNT-----SSSPQPKRKLTDGEYFTLKIRG	337	
		:	: : : : :	
		:	: : : : :	
QY	338	PNKEWLLQSIEGMKEAAAEEVLRNPNQENLRRHANKLLSLK	378	
		:	: : : : :	
		:	: : : : :	
DB	338	QERFKMFQELNEALELKDQAALK--ASEDSGAHSYVLKSCK	376	

RESULT 5
S38824 cellular tumor antigen p53, minor splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38824; S35478
R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Mol. Cell. Biol. 6, 3232-3239, 1986
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
A:Reference number: S38822; MUID:87064640
A:Accession: S38824
A:Molecule type: mRNA
A:Residues: 1-381 <ARA>
A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
R:Han, K.A.; Kulesz-Martin, M.F.
Nucleic Acids Res. 20, 1979-1981, 1992
A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different
A:Reference number: S35478; MUID:92253421
A:Accession: S35478
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-381 <HAN>
A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
C:Comment: This sequence, produced by alternative splicing of the tenth intron, la
s not known.
C:Superfamily: cellular tumor antigen p53
C:Keywords: alternative splicing; phosphoprotein; zinc
F:1-44/Domain: transcription activation #status predicted <TRA>
F:16-26/Region: conserved region I
F:99-289/Domain: DNA-binding core #status predicted <DBC>
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: L2 loop
F:168-178/Region: conserved region III
F:231-252/Region: conserved region IV
F:233-248/Region: L3 loop
F:267-283/Region: conserved region V
F:313-319/Region: nuclear location signal
F:319-357/Region: tetramer association
F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

	Query Match	8.5%;	Score 17.1;	DB 2;	Length 381;
	Best Local Similarity	24.7%;	Pred. No. 2.1e-06;		
Matches	72; Conservative	49; Mismatches	114;	Indels	Gaps
QY	107 YSIPLNKLKLYIRMKAFFNDVQFKSRMPIOPLNLRFVLCF--SNDVSAPVVRCQNHLSVEP	164 : : : : : : : : : : : :			
Dd	123 YSPPLNKLEFFLAKTCPVQL-WVSATPPAGSRVRAMAIYKKSQHMTVEVRRCPHHCRCS-	180 : : : : : : : : : : : :			
QY	165 LTANNAKMRESLLRSENPNPNSVYCNGAQQKGISE---RFSVVVPLNMRSVTRSGLTROT	220 : : : : : : : : : : :			
Dd	181 -DGDGLAPPQHILRVE-----GNLYPEYLEDRTFRHSVVVPY----EPEAGSEYIT	228 : : : : : : : : : : :			
QY	221 LAFKFVCNSCIG---RKETSLVFCEKACGDIQGVIHVKTICTCPKRDRIQDERQIINS	277 : : : : : : : : : : : : : :			

D b	229	IHYKMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVYVACPGDRDRTEENFR-	287
Q Y	278	KRRKSVPEAAEEDPESKVRRCIAKTEDTESNDSRDCDSAAEWNVSRTPDGDYRLAITC	337
D b	288	KKEVLCPEL-----PPGSAKRALPTCT-----SASPQQKKKPLDGEYFTLKIR	330
Q Y	338	PNKEW-----LLQSIEGMIKEAAAEVLNPNQENLRHHANKLLSLKKRAYE	383
D b	331	GRKRFEMFRELNEALE--LKDAHA---TEESGDSRAHS-----SLOPRAFO	371

RESULT 6
DNMS53
cellular tumor antigen p53 - mouse
N;Alternate names: oncoprotein p53
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
A;Reference number: A22739; MUID:85027173
A;Accession: A22739
A;Molecule type: DNA
A;Residues: 1-134,'V',136-390 <BIE>
A;Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237;
R;Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
A;Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
A;Reference number: S06336; MUID:88221682
A;Accession: S06336
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-134,'V',136-390 <CHU>
R;Zakut-Houri, R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum, S.; Givol, D.
Nature 306, 594-597, 1983
A;Title: A single gene and a pseudogene for the cellular tumour antigen p53.
A;Reference number: A02684; MUID:84068204
A;Accession: A02684
A;Molecule type: mRNA
A;Residues: 1-159,'H',161-167,'G',169-233,'I',235-390 <ZAK>
A;Cross-references: GB:X01237; GB:K01700; NID:g53575
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Mol. Cell. Biol. 6, 3232-3239, 1986
A;Title: Immunologically distinct p53 molecules generated by alternative splicing.
A;Reference number: S38822; MUID:87064640
A;Accession: S38822
A;Molecule type: mRNA
A;Residues: 1-390 <ARA1>
A;Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199
A;Accession: S38823
A;Molecule type: mRNA
A;Residues: 1-167,'G',169-233,'I',235-390 <ARA2>
A;Cross-references: EMBL:M13873
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
submitted to the EMBL Data Library, July 1988
A;Reference number: S40014
A;Accession: S40014
A;Molecule type: mRNA
A;Residues: 1-167,'G',169-390 <ARA3>
A;Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; PID:g200201
R;Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
A;Title: Cloning and expression analysis of full length mouse cDNA sequences encoding
A;Reference number: I48703; MUID:84272240
A;Accession: I48703
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-47,'R',49-78,'QW',82-390 <RES>
A;Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA25323.1; PID:g53571
C;Comment: This DNA-binding protein plays an essential role in the regulation of cell
C;Comment: The tetramer association region may exhibit a beta-turn, beta-sheet, beta-
C;Superfamily: cellular tumor antigen p53

1. $\frac{1}{2}$ 2. $\frac{1}{3}$ 3. $\frac{1}{4}$ 4. $\frac{1}{5}$ 5. $\frac{1}{6}$ 6. $\frac{1}{7}$ 7. $\frac{1}{8}$ 8. $\frac{1}{9}$ 9. $\frac{1}{10}$ 10. $\frac{1}{11}$ 11. $\frac{1}{12}$ 12. $\frac{1}{13}$ 13. $\frac{1}{14}$ 14. $\frac{1}{15}$ 15. $\frac{1}{16}$ 16. $\frac{1}{17}$ 17. $\frac{1}{18}$ 18. $\frac{1}{19}$ 19. $\frac{1}{20}$ 20. $\frac{1}{21}$ 21. $\frac{1}{22}$ 22. $\frac{1}{23}$ 23. $\frac{1}{24}$ 24. $\frac{1}{25}$ 25. $\frac{1}{26}$ 26. $\frac{1}{27}$ 27. $\frac{1}{28}$ 28. $\frac{1}{29}$ 29. $\frac{1}{30}$ 30. $\frac{1}{31}$ 31. $\frac{1}{32}$ 32. $\frac{1}{33}$ 33. $\frac{1}{34}$ 34. $\frac{1}{35}$ 35. $\frac{1}{36}$ 36. $\frac{1}{37}$ 37. $\frac{1}{38}$ 38. $\frac{1}{39}$ 39. $\frac{1}{40}$ 40. $\frac{1}{41}$ 41. $\frac{1}{42}$ 42. $\frac{1}{43}$ 43. $\frac{1}{44}$ 44. $\frac{1}{45}$ 45. $\frac{1}{46}$ 46. $\frac{1}{47}$ 47. $\frac{1}{48}$ 48. $\frac{1}{49}$ 49. $\frac{1}{50}$ 50. $\frac{1}{51}$ 51. $\frac{1}{52}$ 52. $\frac{1}{53}$ 53. $\frac{1}{54}$ 54. $\frac{1}{55}$ 55. $\frac{1}{56}$ 56. $\frac{1}{57}$ 57. $\frac{1}{58}$ 58. $\frac{1}{59}$ 59. $\frac{1}{60}$ 60. $\frac{1}{61}$ 61. $\frac{1}{62}$ 62. $\frac{1}{63}$ 63. $\frac{1}{64}$ 64. $\frac{1}{65}$ 65. $\frac{1}{66}$ 66. $\frac{1}{67}$ 67. $\frac{1}{68}$ 68. $\frac{1}{69}$ 69. $\frac{1}{70}$ 70. $\frac{1}{71}$ 71. $\frac{1}{72}$ 72. $\frac{1}{73}$ 73. $\frac{1}{74}$ 74. $\frac{1}{75}$ 75. $\frac{1}{76}$ 76. $\frac{1}{77}$ 77. $\frac{1}{78}$ 78. $\frac{1}{79}$ 79. $\frac{1}{80}$ 80. $\frac{1}{81}$ 81. $\frac{1}{82}$ 82. $\frac{1}{83}$ 83. $\frac{1}{84}$ 84. $\frac{1}{85}$ 85. $\frac{1}{86}$ 86. $\frac{1}{87}$ 87. $\frac{1}{88}$ 88. $\frac{1}{89}$ 89. $\frac{1}{90}$ 90. $\frac{1}{91}$ 91. $\frac{1}{92}$ 92. $\frac{1}{93}$ 93. $\frac{1}{94}$ 94. $\frac{1}{95}$ 95. $\frac{1}{96}$ 96. $\frac{1}{97}$ 97. $\frac{1}{98}$ 98. $\frac{1}{99}$ 99. $\frac{1}{100}$ 100. $\frac{1}{101}$ 101. $\frac{1}{102}$ 102. $\frac{1}{103}$ 103. $\frac{1}{104}$ 104. $\frac{1}{105}$ 105. $\frac{1}{106}$ 106. $\frac{1}{107}$ 107. $\frac{1}{108}$ 108. $\frac{1}{109}$ 109. $\frac{1}{110}$ 110. $\frac{1}{111}$ 111. $\frac{1}{112}$ 112. $\frac{1}{113}$ 113. $\frac{1}{114}$ 114. $\frac{1}{115}$ 115. $\frac{1}{116}$ 116. $\frac{1}{117}$ 117. $\frac{1}{118}$ 118. $\frac{1}{119}$ 119. $\frac{1}{120}$ 120. $\frac{1}{121}$ 121. $\frac{1}{122}$ 122. $\frac{1}{123}$ 123. $\frac{1}{124}$ 124. $\frac{1}{125}$ 125. $\frac{1}{126}$ 126. $\frac{1}{127}$ 127. $\frac{1}{128}$ 128. $\frac{1}{129}$ 129. $\frac{1}{130}$ 130. $\frac{1}{131}$ 131. $\frac{1}{132}$ 132. $\frac{1}{133}$ 133. $\frac{1}{134}$ 134. $\frac{1}{135}$ 135. $\frac{1}{136}$ 136. $\frac{1}{137}$ 137. $\frac{1}{138}$ 138. $\frac{1}{139}$ 139. $\frac{1}{140}$ 140. $\frac{1}{141}$ 141. $\frac{1}{142}$ 142. $\frac{1}{143}$ 143. $\frac{1}{144}$ 144. $\frac{1}{145}$ 145. $\frac{1}{146}$ 146. $\frac{1}{147}$ 147. $\frac{1}{148}$ 148. $\frac{1}{149}$ 149. $\frac{1}{150}$ 150. $\frac{1}{151}$ 151. $\frac{1}{152}$ 152. $\frac{1}{153}$ 153. $\frac{1}{154}$ 154. $\frac{1}{155}$ 155. $\frac{1}{156}$ 156. $\frac{1}{157}$ 157. $\frac{1}{158}$ 158. $\frac{1}{159}$ 159. $\frac{1}{160}$ 160. $\frac{1}{161}$ 161. $\frac{1}{162}$ 162. $\frac{1}{163}$ 163. $\frac{1}{164}$ 164. $\frac{1}{165}$ 165. $\frac{1}{166}$ 166. $\frac{1}{167}$ 167. $\frac{1}{168}$ 168. $\frac{1}{169}$ 169. $\frac{1}{170}$ 170. $\frac{1}{171}$ 171. $\frac{1}{172}$ 172. $\frac{1}{173}$ 173. $\frac{1}{174}$ 174. $\frac{1}{175}$ 175. $\frac{1}{176}$ 176. $\frac{1}{177}$ 177. $\frac{1}{178}$ 178. $\frac{1}{179}$ 179. $\frac{1}{180}$ 180. $\frac{1}{181}$ 181. $\frac{1}{182}$ 182. $\frac{1}{183}$ 183. $\frac{1}{184}$ 184. $\frac{1}{185}$ 185. $\frac{1}{186}$ 186. $\frac{1}{187}$ 187. $\frac{1}{188}$ 188. $\frac{1}{189}$ 189. $\frac{1}{190}$ 190. $\frac{1}{191}$ 191. $\frac{1}{192}$ 192. $\frac{1}{193}$ 193. $\frac{1}{194}$ 194. $\frac{1}{195}$ 195. $\frac{1}{196}$ 196. $\frac{1}{197}$ 197. $\frac{1}{198}$ 198. $\frac{1}{199}$ 199. $\frac{1}{200}$ 200. $\frac{1}{201}$ 201. $\frac{1}{202}$ 202. $\frac{1}{203}$ 203. $\frac{1}{204}$ 204. $\frac{1}{205}$ 205. $\frac{1}{206}$ 206. $\frac{1}{207}$ 207. $\frac{1}{208}$ 208. $\frac{1}{209}$ 209. $\frac{1}{210}$ 210. $\frac{1}{211}$ 211. $\frac{1}{212}$ 212. $\frac{1}{213}$ 213. $\frac{1}{214}$ 214. $\frac{1}{215}$ 215. $\frac{1}{216}$ 216. $\frac{1}{217}$ 217. $\frac{1}{218}$ 218. $\frac{1}{219}$ 219. $\frac{1}{220}$ 220. $\frac{1}{221}$ 221. $\frac{1}{222}$ 222. $\frac{1}{223}$ 223. $\frac{1}{224}$ 224. $\frac{1}{225}$ 225. $\frac{1}{226}$ 226. $\frac{1}{227}$ 227. $\frac{1}{228}$ 228. $\frac{1}{229}$ 229. $\frac{1}{230}$ 230. $\frac{1}{231}$ 231. $\frac{1}{232}$ 232. $\frac{1}{233}$ 233. $\frac{1}{234}$ 234. $\frac{1}{235}$ 235. $\frac{1}{236}$ 236. $\frac{1}{237}$ 237. $\frac{1}{238}$ 238. $\frac{1}{239}$ 239. $\frac{1}{240}$ 240

A;Cross-references: EMBL:M14694; NID:q339813; PIDN:AAA61211.1; PID:q339814


```

Query Match          7.6%; Score 152; DB 1; Length 393;
Best Local Similarity 22.7%; Pred. No. 8e-05;
Matches 64; Conservative 50; Mismatches 124; Indels 44; Gaps 11;

QY  107 YSIPLNKLYIRMNKAFFVDVQFKSKMPIQLNLRYFLCF--SNDVSAPVVRCQNHL SVEP 164
Db   126 YSPDLNMKFCQLAKTCPVOLWVDSTPP-PGSRVRAMAIYKQSQHMTFVRRCPHHERCS- 183
QY  165 LTANNAKMRESLLRSENPNFSVCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT 220
Db   184 -DSDGLAPPQOHLIRVE-----GNLRVEYSDDRNTFRHSVVVPY-----EPPEVGSDCTT 231
QY  221 LAFKFVCQNSCIG---RKETSLVFLEKACGDIVGHVHVKTCTPKRDRIQDERQLNS 277
Db   232 IHNYMCMSSCMGMNRRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTTEENFRK 291
QY  278 KKRKSVPAAEEDEPSKVRRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAIT 336
Db   292 K-----GEPCHLPFGSKRALPNNT-----SSSQPKKKPLDGGEYFTLQIR 333
QY  337 CPNKEWLLQSTEGMIKEAAAFAVLNPQENLRRHANKLLSLK 378
Db   334 GRGFEMFRELNEALELKDAQAGKEP--AGSRAHSSHLSKSK 373

RESULT 13
T05687
beta-galactosidase homolog F20M13.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000
C:Accession: T05687
R;Bevan, M.; Wedler, H.; Kutznier, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.E. et al., 1994
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15420
A:Accession: T05687
A:Molecule type: DNA
A:Residues: 1-1036 <BEV>
A:Cross-references: EMBL:AL035540
A:Experimental source: cultivar Columbia; BAC clone F20M13
C:Genetics:
```

A:Reference number: S55680; MUID:95322425
 A:Accession: S55680
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1569-1582 <YAM>
 R:Van het Schip, F.D.; Samallo, J.; Broos, J.; Ophuis, J.; Mojet, M.; Gruber, M.; AB, J. Mol. Biol. 196, 245-260, 1987
 A:Title: Nucleotide sequence of a chicken vitellogenin gene and derived amino acid se
 A:Reference number: A92941; MUID:88011328
 A:Accession: A92941
 A:Molecule type: DNA
 A:Residues: 1-579,582-774,'R',776-1138,'S',1140-1437,'HK',1440-1852 <VAN>
 A:Cross-references: GB:X13607; NID:g63886; PIDN:CAA31942.1; PID:g63887
 A:Note: 1842-Ala was also found
 R:Burch, J.B.E.
 Nucleic Acids Res. 12, 1117-1135, 1984
 A:Title: Identification and sequence analysis of the 5' end of the major chicken vite
 A:Reference number: A93502; MUID:84118805


```

QY 226 VQNSCIGRKETSLVFCLEKACGDIVGQH---VIHVKICTPKRDRIOQERQLNSKKRKS 282
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 998 IGCQLCFRRSRDASFIQNTYLHKLIGEHEAKIVLMPVHTDADIDKIQLEIQAGSRAAR 1057
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :

QY 283 V-----PEAAEEDPS-----KVRRCIAI-----KTEDTESNDSR----- 312
   : | | : | | | | | | | | : | | : | | : | | : | | : | | : | | :
Db 1058 IITEVNPESSEEDDESSPYEDIQAKLKRILGIDSMFKVANKTRHPKPNRPSKKGNTVLAEEG 1117
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :

QY 313 ---DCDDSAAEWNVSRTPDGYRLAITCPNKEWLL-----QSIEGMIKEAAAEVLRPN 363
   | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1118 TEPDAKTSSSSSASSTATSSASSASSPNRKKPMDEEENDQVKQARNKDASSSSRSK 1177
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :

QY 364 QENLRRHANKLLSLKKRA 381
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1178 SNSSKRSSSKSSNSSKRS 1195
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :

RESULT 15
D96703
hypothetical protein T23K23.12 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C/Accession: D96703
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
ansen, N.F.; Hughes, B.; Huizlar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719
A/Accession: D96703
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-314 <STO>
A/Cross-references: GB:AE005173; NID:g6553893; PIDN:AAF16559.1; GSPDB:GN00141
C/Genetics:
A/Gene: T23K23.12
A/Map position: 1

Query Match 5.2%; Score 103.5; DB 2; Length 314;
Best Local Similarity 21.4%; Pred. No. 0.57;
Matches 66; Conservative 42; Mismatches 99; Indels 101; Gaps 1

QY 24 DIKEDIPKTVESGSELTTEPMAF--LQGLNSGNLMQFSQSVLRMLQDIQANTLP 81
   | : | | | : | | | | | | | | | | : | : | : | : | :
Db 42 DVFELAPKLDPYLG-EYTNEMVAFRCLASLFDHSHVSVTTTTTTTSMI----- 88
   : : : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 82 KLENHNIGGYCFSMVLDEPPKSLMWYSIPLNKLIRMNKAFNVQFKSKMP-IQPLNLR 140
   : : : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89 EEDSSECEYVLQILDE-----IPLSEL-----KPGAPGLTKWNLQ 125
   : : : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 141 VFLCFSDNVSAPVVRCONHLSVEPLTANNKM-----RESLLRSENPNSVYCGNAQKGKI 195
   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 126 PFIKHKL-LSLP--KCALELMIEPSSCENDIQVSPCSEETLRSD-----GK-- 169
   : : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :

QY 196 SERFSVVVPLN-----MSRSVTRSG---LTRQTIAFKFVCQNS----- 230
   | | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 170 -ENDRVTPPMDEPDLTGRTEGESFSRGADELDRRNAGFRYESENDSGLHSSPVEKIYR 228
   : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | :

QY 231 CTGRKET-SLVFCLEKACGDIVGQHV-----HVKIC--TCPKRDRIQDERQL 275
   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 229 CVNCKESGKLLFCSSDGCVEVMVHQCLDSPPSYHDAGDFYCSLCALTCPSAEYVQFQDEV 288
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :

QY 276 NSKKRKSV 283
   | | | |
Db 289 AKAKRKLV 296
   | | | |

```


Search completed: November 16, 2001, 15:50:51
Job time: 2443 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 16, 2001, 15:49:08 ; Search time 32.01 Seconds
(without alignments)
412.008 Million cell updates/sec

Title: US-09-524-101-2

Perfect score: 2008

Sequence: 1 MYISQPMWHKSTSEDDSDS.....NLRHANKLLSLKRAYELP 385

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	201	10.0	342	1	P53_XIPHE
2	199	9.9	342	1	P53_XIPMA
3	191	9.5	636	1	P73_HUMAN
4	190	9.5	637	1	P73_CERAE
5	183.5	9.1	381	1	P53_CANFA
6	183	9.1	391	1	P53_RAT
7	182.5	9.1	386	1	P53_FELCA
8	181	9.0	366	1	P53_PLAFE
9	180.5	9.0	386	1	P53_BOVIN
10	179	8.9	367	1	P53_TETMU
11	176.5	8.8	363	1	P53_XENLA
12	176.5	8.8	386	1	P53_PIG
13	174	8.7	396	1	P53_MESAU
14	173.5	8.6	376	1	P53_ICTPU
15	170.5	8.5	280	1	P53_HORSE
16	170	8.5	369	1	P53_BARBU
17	168.5	8.4	390	1	P53_MOUSE
18	168	8.4	314	1	P53_SPEBE
19	168	8.4	367	1	P53_CHICK
20	168	8.4	393	1	P53_CRIGR
21	166.5	8.3	207	1	P53_EQUAS
22	166.5	8.3	382	1	P53_SHEEP
23	166	8.3	391	1	P53_MARMO
24	165.5	8.2	391	1	P53_RABIT
25	165	8.2	351	1	P53_ORYLA
26	165	8.2	391	1	P53_CAVPO
27	164.5	8.2	396	1	P53_ONCMY
28	160	8.0	393	1	P53_HUMAN
29	152	7.6	393	1	P53_CERAE
30	150	7.5	393	1	P53_TUPGB
31	149	7.4	393	1	P53_MACFA
32	149	7.4	393	1	P53_MACMU
33	142	7.1	373	1	P53_BRARE

34	111	5.5	1850	1	VIT2_CHICK	P02845	gallus galli
35	98.5	4.9	612	1	UN37_CAEEL	O02482	caenorhabdi
36	97.5	4.9	1148	1	CNN_DROME	P54623	drosophila
37	96.5	4.8	687	1	DB73_DROME	P26802	drosophila
38	95.5	4.8	3321	1	KEND_HUMAN	O95613	homo sapien
39	95	4.7	1394	1	HAP_HAEIN	P45387	haemophilus
40	94.5	4.7	697	1	SP3_HUMAN	Q02447	homo sapien
41	94	4.7	1244	1	YP83_CAEEL	Q09441	caenorhabdi
42	93	4.6	1274	1	SRF3_BACSU	Q08787	bacillus su
43	90.5	4.5	1228	1	ECM_HUMAN	Q13201	homo sapien
44	89.5	4.5	232	1	PROQ_ECOLI	P45577	escherichia
45	89.5	4.5	2025	1	TTC3_HUMAN	P53804	homo sapien

ALIGNMENTS

RESULT 1
P53_XIPHE
ID P53_XIPHE STANDARD; PRT; 342 AA.
AC O57538;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Xiphophorus helleri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_TaxID=8084;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIO SARAFIA;
RX MEDLINE=9832630;; PubMed=9661661;
RA Kazianis S., Gan L., Della Coletta L., Santi B., Morizot D.C.,
RA Nairn R.S.;
RT "Cloning and comparative sequence analysis of TP53 in xiphophorus fish
hybrid melanoma models.";
RL Gene 212:31-38(1998).
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
EXPRESSON (BY SIMILARITY).
CC -!- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
CC EMBL; AF043946; AAC31133.1; -.
DR HSSP; P04637; 1TSR.
DR InterPro; IPR002117; -.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; DNA phosphorylation; Apoptosis.
FT DOMAIN 1 35 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 68 255 BY SIMILARITY.

RA Minty A., Chalon P., Lelias J.-M., Dumont X., Ferrara P., McKeon F.,
RA Caput D.;
RT "Monoallelically expressed gene related to p53 at lp36, a region
RT frequently deleted in neuroblastoma and other human cancers.";
RL Cell 90:809-819(1997).
RN [2];
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=99289209; PubMed=10362303;
RA Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K.,
RA Harris C.C.;
RT "Mutational analysis of p73 and p53 in human cancer cell lines.";
RL Oncogene 18:3415-3421(1999).
RN [3];
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98389621; PubMed=9721206;
RA Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,
RA Jenkins R., Smith D.I., Liu W.;
RT "Genomic organization and mutation analysis of p73 in
RT oligodendrogliomas with chromosome 1 p-arm deletions.";
RL Genomics 51:359-363(1998).
RN [4];
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).
RC TISSUE=Neuroblastoma;
RX MEDLINE=99021697; PubMed=9802988;
RA De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,
RA Annicchiarico-Petruzzelli M., Levvero M., Melino G.;
RT "Two new p73 splice variants, gamma and delta, with different
RT transcriptional activity.";
RL J. Exp. Med. 188:1763-1768(1998).
RN [5];
RP SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).
RC TISSUE=Lymphocytes, Breast cancer, Hepatoma, and Skin;
RX MEDLINE=99310938; PubMed=10381648;
RA De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G.,
RA Costanzo A., Levvero M., Knight R.A.;
RT "Additional complexity in p73: induction by mitogens in
RT and identification of two new splicing variants epsilon and zeta.";
RL Cell Death Differ. 6:389-390(1999).
RN [6];
RP SEQUENCE FROM N.A. (ISOFORM KAPPA).
RA Thomas D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [7];
RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
RX MEDLINE=99318135; PubMed=10391251;
RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RA Kharbanda S., Weichselbaum R., Kufe D.;
RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
RT to DNA damage.";
RL Nature 399:814-817(1999).
RN [8];
RP ERRATUM.
RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RA Kharbanda S., Weichselbaum R., Kufe D.;
RL Nature 400:792-792(1999).
RN [9];
RP FUNCTION.
RX MEDLINE=99217940; PubMed=10203277;
RA Kaelin W.G. Jr.;
RT "The emerging p53 gene family.";
RL J. Natl. Cancer Inst. 91:594-598(1999).
RN [10];
RP STRUCTURE BY NMR OF 439-506.
RX MEDLINE=99380160; PubMed=10449409;
RA Chi S.W., Ayed A., Arrowsmith C.H.;
RT "Solution structure of a conserved C-terminal domain of p73 with
RT structural homology to the SAM domain.";
RL EMBO J. 18:4438-4445(1999).
CC -!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
CC PROTEIN.
CC -!- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL

CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- ALTERNATIVE PRODUCTS: 7 ISOFORMS; ALPHA (SHOWN HERE), BETA, GAMMA,
CC DELTA, EPSILON, ZETA AND KAPPA; ARE PRODUCED BY ALTERNATIVE
CC SPLICING. THE SPLICING OF EXON 11 IN GAMMA AND EPSILON ISOFORMS
CC RESULTS IN A FRAMESHIFT FROM THE ORIGINAL READING FRAME. THE
CC SPLICING OF EXON 13 IN EPSILON ISOFORM REVERTS THE READING FRAME
CC TO THE ALPHA ISOFORM.
CC -!- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
CC -!- INDUCTION: NOT INDUCED BY DNA DAMAGE.
CC -!- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
CC -!- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE
CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y11416; CAA72220.1; -;
DR EMBL; Y11416; CAA72221.1; -;
DR EMBL; Y11416; CAA72219.1; -;
DR EMBL; AF077628; AAC61887.1; -;
DR EMBL; AF077616; AAC61887.1; JOINED.
DR EMBL; AF077617; AAC61887.1; JOINED.
DR EMBL; AF077618; AAC61887.1; JOINED.
DR EMBL; AF077619; AAC61887.1; JOINED.
DR EMBL; AF077620; AAC61887.1; JOINED.
DR EMBL; AF077621; AAC61887.1; JOINED.
DR EMBL; AF077624; AAC61887.1; JOINED.
DR EMBL; AF077625; AAC61887.1; JOINED.
DR EMBL; AF077626; AAC61887.1; JOINED.
DR EMBL; AF077627; AAC61887.1; JOINED.
DR EMBL; AF079094; AAD39696.1; -;
DR EMBL; AF079082; AAD39696.1; JOINED.
DR EMBL; AF079083; AAD39696.1; JOINED.
DR EMBL; AF079084; AAD39696.1; JOINED.
DR EMBL; AF079085; AAD39696.1; JOINED.
DR EMBL; AF079086; AAD39696.1; JOINED.
DR EMBL; AF079087; AAD39696.1; JOINED.
DR EMBL; AF079088; AAD39696.1; JOINED.
DR EMBL; AF079089; AAD39696.1; JOINED.
DR EMBL; AF079090; AAD39696.1; JOINED.
DR EMBL; AF079091; AAD39696.1; JOINED.
DR EMBL; AF079092; AAD39696.1; JOINED.
DR EMBL; AF079093; AAD39696.1; JOINED.
DR EMBL; AL136528; CAB92742.1; -;
DR PDB; 1COK; 17-AUG-99.
DR MIM; 601990; -;
DR InterPro; IPR002117; -;
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Transcription regulation; Activator; DNA-binding; Anti-oncogene;
KW Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;
KW 3D-structure.
FT DOMAIN 1 46 TRANSACTIVATION (BY SIMILARITY).
FT DOMAIN 1 55 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 287 304 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 346 435 MEDIATES OLIGOMERIZATION (POTENTIAL).
FT DOMAIN 168 171 POLY-PRO.

ID AC Q29537; Q9TV78; STANDARD; PRT; 381 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=98178696; PubMed=9519881;
RA Veldhoen N., Milner J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the
full length canine p53 protein.";
RL Oncogene 16:1077-1084(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA Watari T., Hasagawa A., Tsujimoto H.;
RT "Aberrations of p53 tumor suppressor gene in various spontaneous
tumors in the dog.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-300 FROM N.A.
RC STRAIN=BEAGLE;
RX MEDLINE=95323915; PubMed=7600529;
RA Kraegel S.A., Pazzi K.A., Madewell B.R.;
RT "Sequence analysis of canine p53 in the region of exons 3-8.";
RL Cancer Lett. 92:181-186(1995).
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
EXPRESSION.
CC -!- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL; AF060514; AAC16909.1; -
DR EMBL; AB020761; BAA78379.1; -
DR EMBL; S77819; AAB42022.1; -
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; -
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 89 280 BY SIMILARITY.
FT DOMAIN 313 344 OLIGOMERIZATION.
FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).

FT DOMAIN 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 2 4 EES -> QEP (IN REF. 2).
FT CONFLICT 378 378 L -> P (IN REF. 2).
SQ SEQUENCE 381 AA; 42486 MW; 761A718FDC93DA59 CRC64;

Query Match 9.1%; Score 183.5; DB 1; Length 381;
Best Local Similarity 23.3%; Pred. No. 7.1e-08;
Matches 66; Conservative 45; Mismatches 109; Indels 63; Gaps 11;

QY 105 WMYSIPLNKLKLYIRMKAFNVVDVQFKSKMPIQLNLRVFLCF--SNDVSAPVVRQNHLSV 162
Db 111 WTYSPLLNKLFQCLAKTCPVQLWVSSPPPPNTC-VRAMAIYKKSEFTEVVRCPHHERC 169
QY 163 EPLTANNAKMRESLLRSENPNVYCGNAQKGISE----RFSVVVPLNMSRSTRSGLTR 218
Db 170 SD-SSDGLAPPQHLIRVE-----GNLRKYLDRNTFRHSVVVPPY----EPPEVGSDY 217
QY 219 QTLAFKFCVQNSCIG---RKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIDRQL 275
Db 218 TTIHYNYMCNSSCMGNNRRPILITITLEDSSGNVLGRNSFEVRVCACPGDRDRTEENF 277
QY 276 NSKKRKSVPAAEEDPSKVRRCIAKTEDTESNDSRDCDDSAAEWNVSRTPDGYRLAI 335
Db 278 HKK-----GEPCEPPPGSTKRALPPSTSSSPQKKKPL-----DGEY---- 315
QY 336 TPCNKEWLLQSIEMIKAEAAAEVLRNPQNENLRHANKLLSLK 378
Db 316 -----FTLQ-----INGRERYEMFRNLNEALELK 339

RESULT 6

P53_RAT
ID P53_RAT STANDARD; PRT; 391 AA.
AC P10361; O09168;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89083585; PubMed=3060862;
RA Soussi T.;
RT "Nucleotide sequence of a cDNA encoding the rat p53 nuclear
oncoprotein.";
RL Nucleic Acids Res. 16:11384-11384(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93181268; PubMed=8441680;
RA Hulla J.E., Schneider R.P.;
RT "Structure of the rat p53 tumor suppressor gene.";
RL Nucleic Acids Res. 21:713-717(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Mathupala S.P.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
EXPRESSION.

Db 332 DLLENKPKSKATHRPDG 348

RESULT 11

P53_XENLA

ID P53_XENLA STANDARD; PRT; 363 AA.

AC P07193;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).

GN TP53.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88143684; PubMed=2830576;

RA Soussi T., de Fromental C.C., Mechali M., May P., Kress M.;

RT "Cloning and characterization of a cDNA from xenopus laevis coding for a protein homologous to human and murine p53."

RL Oncogene 1:71-78(1987).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=94134403; PubMed=8302570;

RA Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.;

RT "Overexpression of wild-type p53 interferes with normal development in Xenopus laevis embryos."

RL Oncogene 9:109-120(1994).

CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).

CC -!- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: NUCLEAR.

CC -!- TISSUE SPECIFICITY: UBIQUITOUS.

CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; M36962; AAA49923.1; -

EMBL; X05191; CAA28821.1; -

EMBL; X77546; CAA54672.1; -

EMBL; S68353; AAC60746.1; -

PIR; A29376; A29376.

HSSP; P04637; ITR.

InterPro; IPR002117; -

Pfam; PF00870; P53; 1.

PRINTS; PR00386; P53SUPPRESSR.

PROSITE; PS00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;

KW Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).

FT DNA_BIND 76 267 BY SIMILARITY.

FT DOMAIN 300 331 OLIGOMERIZATION.

FT DOMAIN 344 356 BASIC (REPRESSION OF DNA-BINDING).

FT DOMAIN 281 293 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT MOD_RES 362 362 PHOSPHORYLATION (BY SIMILARITY).

FT CONFLICT 52 52 T -> S (IN REF. 2).

FT CONFLICT 71 71 MISSING (IN REF. 2).

FT CONFLICT 296 296 MISSING (IN REF. 2).

SQ SEQUENCE 363 AA; 40692 MW; CELF3E58F020D74D CRC64;

Query Match 8.8%; Score 176.5; DB 1; Length 363;

Best Local Similarity 26.2%; Pred. No. 2.5e-07;

Matches 73; Conservative 46; Mismatches 119; Indels 41; Gaps 13;

QY 55 NLMQFSQSVLREMLQDIQIQANTLPKLENHNI-----GGYCFSMVLDE--PPKSL- 104

Db 38 NLSEFPDYPPLAADMVTLQEGLMGNVPTVTSCAVPSTDDYAGKYGLQDFQNGTAKSVT 97

QY 105 WMYSIPLNKLIRMNKAFNVQFKSKMPIQLNLRVFLCF--SNDVSAPVVRCONH-LS 161

Db 98 CTYSPELNKLFQCLAKTCPLLRVVESSPPRSGI-LRATAVYKKSEHVAEVVKKRCPHHERS 156

QY 162 VEPLTANNAKMRRESLLRSENPNVYCGNAQKGI----SERFSVVVPLNMSRSTRSGLT 217

Db 157 VEP--GEDAAPPSHLMRVE-----GNLQAYMEDVNSGRHSCVCPY----EGPQVGTE 203

QY 218 RQTLAEKFCVQNSCIG---RKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIQDERQ 274

Db 204 CTTVLNVMCMSSCMGMNRRPILITITLTPQGLLGRRCFEVRVCACPGDR-RTEED 262

QY 275 LNSKKRKSVPAAEE-----DEPSKVRRCIAIKTEDTE 307

Db 263 NYTKRGLKPSGKRELAHPSPSEPLPKRLVVDDEE 301

RESULT 12

P53_PIG

ID P53_PIG STANDARD; PRT; 386 AA.

AC Q9TUB2;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).

GN TP53 OR P53.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;

RT "Nucleotide sequence of the pig p53 tumor suppressor cDNA";

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION.

CC -!- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: NUCLEAR.

CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.

CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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Search completed: November 16, 2001, 15:56:50
Job time: 462 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 16, 2001, 15:49:53 ; Search time 65.26 Seconds
(without alignments)
780.531 Million cell updates/sec

Title: US-09-524-101-2
Perfect score: 2008
Sequence: 1 MYISQPMWKESTSEDDSS.....NLRHANKLLSLKRAYELP 385

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_16.*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2008	100.0	385	5 Q9N6D8	Q9n6d8 drosophila
2	233.5	11.6	621	5 Q9NGC7	Q9ngc7 mya arenari
3	231.5	11.5	443	5 Q9NGC8	Q9ngc8 mya arenari
4	209	10.4	564	5 Q27937	Q27937 loligo forb
5	199.5	9.9	631	11 Q9UJP2	Q9jjp2 mus musculus
6	186	9.3	448	4 Q76078	Q76078 homo sapien
7	186	9.3	471	4 Q9NPH7	Q9nph7 homo sapien
8	186	9.3	487	4 Q9H3D2	Q9h3d2 homo sapien
9	186	9.3	516	4 Q9UP27	Q9up27 homo sapien
10	186	9.3	516	4 Q9P1B7	Q9plb7 homo sapien
11	186	9.3	555	4 Q9H3D3	Q9h3d3 homo sapien
12	186	9.3	641	4 Q9UP28	Q9up28 homo sapien
13	186	9.3	641	4 Q75195	Q75195 homo sapien
14	186	9.3	680	4 Q9UE10	Q9ue10 homo sapien
15	186	9.3	680	4 Q9H3D4	Q9h3d4 homo sapien
16	185	9.2	555	11 Q9QWZ0	Q9q wz0 mus musculu
17	185	9.2	680	11 Q88898	Q88898 mus musculu
18	183.5	9.1	281	6 Q29475	Q29475 canis famil
19	183	9.1	680	11 Q9UJP6	Q9jjp6 rattus norv

20	182	9.1	461	11 Q9QWY9	Q9qwy9 mus musculu
21	182	9.1	586	11 Q89097	Q89097 mus musculu
22	181.5	9.0	246	6 Q9TUX4	Q9tux4 canis famil
23	181	9.0	483	11 Q88897	Q88897 mus musculu
24	178	8.9	356	4 Q9UP74	Q9up74 homo sapien
25	178	8.9	389	11 Q88899	Q88899 mus musculu
26	178	8.9	393	4 Q75922	Q75922 homo sapien
27	178	8.9	416	4 Q9P1B6	Q9plb6 homo sapien
28	178	8.9	461	4 Q9P1B5	Q9plb5 homo sapien
29	178	8.9	461	4 Q9UP26	Q9up26 homo sapien
30	178	8.9	586	4 Q75080	Q75080 homo sapien
31	178	8.9	586	4 Q9P1B4	Q9plb4 homo sapien
32	178	8.9	586	4 Q9UBV9	Q9ubv9 homo sapien
33	177	8.8	582	13 Q9DEC7	Q9dec7 gallus gall
34	169	8.4	641	13 Q9W664	Q9w664 barbus barb
35	168.5	8.4	390	11 Q70366	Q70366 mus musculu
36	168	8.4	501	4 Q9H3P8	Q9h3p8 homo sapien
37	167.5	8.3	205	11 Q35873	Q35873 cricetus
38	167	8.3	238	14 P89004	P89004 mastomys na
39	167	8.3	286	14 P90332	P90332 mastomys na
40	167	8.3	378	14 P89002	P89002 mastomys na
41	166.5	8.3	387	6 Q9N252	Q9n252 sus scrofa
42	165	8.2	352	13 Q9PSU8	Q9psu8 oryzias lat
43	165	8.2	590	11 Q9JJP1	Q9jjp1 mus musculu
44	164	8.2	286	14 P89003	P89003 mastomys na
45	163	8.1	307	11 Q9ER40	Q9er40 mus musculu

ALIGNMENTS

RESULT	1
Q9N6D8	
ID	Q9N6D8 PRELIMINARY; PRT; 385 AA.
AC	Q9N6D8; Q9VCR8;
DT	01-OCT-2000 (Tremblrel. 15, Created)
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE	TRANSCRIPTION FACTOR P53 (P53 TUMOR SUPPRESSOR-LIKE PROTEIN) (P53 PROTEIN).
DE	P53 OR CG10873.
GN	Drosophila melanogaster (Fruit fly).
OS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
[1]	SEQUENCE FROM N.A.
RP	MEDLINE=20239130; PubMed=10778859;
RX	Ollmann M., Young L.M., Di Como C.J., Karim F., Belvin M.,
RA	Robertson S.A., Whittaker K., Densky M., Fisher W.W., Buchman A.,
RA	Duyk G., Friedman L., Prives C., Kopczyński C.;
RT	"Drosophila p53 is a structural and functional homolog of the tumor suppressor p53.";
RL	Cell 101:91-101(2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20239131; PubMed=10778860;
RA	Brodsky M.H., Nordstrom W., Tsang G., Kwan E., Rubin G.M.,
RA	Abrams J.M.;
RT	"Drosophila p53 binds a damage response element at the reaper locus.";
RL	Cell 101:103-113(2000).
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Potter C.J., Xu T.;
RT	"The identification and characterization of Drosophila melanogaster p53.";
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20319021; PubMed=10860994;
RA	Jin S., Martinek S., Joo W.S., Wortman J.R., Mirkovic N., Sali A.,
RA	Yandell M.D., Pavletich N.P., Young M.W., Levine A.J.;

QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPAAEEDEPSK 294
Db 341 EARICACPGDRKRADE--DSIRKQVSDSTKNGDGTK 375

RESULT 12
Q9UP28 PRELIMINARY; PRT; 641 AA.

AC Q9UP28;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE TA P63 ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
DR EMBL; AF075430; AAC62635.1; -.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR001660; -.
DR InterPro; IPR002117; -.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR SMART; SM00454; SAM; 1.
SQ SEQUENCE 641 AA; 72049 MW; 23A2E5EBAE63F605 CRC64;

Query Match 9.3%; Score 186; DB 4; Length 641;
Best Local Similarity 22.2%; Pred. No. 4.7e-08;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMSWHKESTDSDST-EVDIKEDIPKTVESGSELTTEPMAFLQGLNSGNLMQFSQQS 63
Db 31 QPIDLNFVDEPSEDGATNKIEISMD---CIRMQDSDL-SDPM-----WPQYTNLG 76

QY 64 VLRMMMLQDIQIQ---ANTLPKLENH-----NI 88
Db 77 LLNSM---DQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSTNDYP 133

QY 89 GGYCFSMVLDE---PPKSLMYSIPLNKLIRMNKAFNVQVQFSKMPQIPLNLRVFLCF 145
Db 134 GPHSFDVSFQSQSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 192

QY 146 --SNDVSAPVVRQNHLSVEPLTANNKMRSLRSENPNNSVYCGNAQKGISE----RF 199
Db 193 KKAHVTEVVKRCPNHLSREFNEGQIAPPFSLIRVE-----GNSHAQYVEDPITGRQ 245

QY 200 SVVVPLNMSRVSRTSGLTRQTLAFKVCQNSCIG---RKETSLVFCLEKACGDIVGQHV 256
Db 246 SVLVPIY---EPPQVGTEFTTVLYNFMNCSVCGVMNRRPILIIIVTLETRDQGVLRRCF 301

QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPAAEEDEPSK 294
Db 302 EARICACPGDRKRADE--DSIRKQVSDSTKNGDGTK 336

RESULT 13
O75195 PRELIMINARY; PRT; 641 AA.

AC O75195;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE P51 ISOFORM TAP63ALPHA (P51B PROTEIN).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKELETAL MUSCLE;
RX MEDLINE=98324755; PubMed=9662378;
RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawara A., Obinata M.;
RT "Cloning and functional analysis of human p51, which structurally and
RT functionally resembles p53";
RL Nat. Med. 4:839-844(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
DR EMBL; AB016073; BAA32593.1; -.
DR EMBL; AF116769; AAF43487.1; -.
DR EMBL; AF116756; AAF43487.1; JOINED.
DR EMBL; AF116757; AAF43487.1; JOINED.
DR EMBL; AF116759; AAF43487.1; JOINED.
DR EMBL; AF116760; AAF43487.1; JOINED.
DR EMBL; AF116761; AAF43487.1; JOINED.
DR EMBL; AF116762; AAF43487.1; JOINED.
DR EMBL; AF116763; AAF43487.1; JOINED.
DR EMBL; AF116764; AAF43487.1; JOINED.
DR EMBL; AF116765; AAF43487.1; JOINED.
DR EMBL; AF116766; AAF43487.1; JOINED.
DR EMBL; AF116767; AAF43487.1; JOINED.
DR EMBL; AF116768; AAF43487.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; -.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; -.
SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;

Query Match 9.3%; Score 186; DB 4; Length 641;
Best Local Similarity 22.2%; Pred. No. 4.7e-08;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMSWHKESTDSDST-EVDIKEDIPKTVESGSELTTEPMAFLQGLNSGNLMQFSQQS 63
Db 31 QPIDLNFVDEPSEDGATNKIEISMD---CIRMQDSDL-SDPM-----WPQYTNLG 76

QY 64 VLRMMMLQDIQIQ---ANTLPKLENH-----NI 88
Db 77 LLNSM---DQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSTNDYP 133

QY 89 GGYCFSMVLDE---PPKSLMYSIPLNKLIRMNKAFNVQVQFSKMPQIPLNLRVFLCF 145
Db 134 GPHSFDVSFQSQSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 192

QY 146 --SNDVSAPVVRQNHLSVEPLTANNKMRSLRSENPNNSVYCGNAQKGISE----RF 199
Db 193 KKAHVTEVVKRCPNHLSREFNEGQIAPPFSLIRVE-----GNSHAQYVEDPITGRQ 245

QY 200 SVVVPLNMSRVSRTSGLTRQTLAFKVCQNSCIG---RKETSLVFCLEKACGDIVGQHV 256
Db 246 SVLVPIY---EPPQVGTEFTTVLYNFMNCSVCGVMNRRPILIIIVTLETRDQGVLRRCF 301

QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPAAEEDEPSK 294
Db 302 EARICACPGDRKRADE--DSIRKQVSDSTKNGDGTK 336

RESULT 14
Q9UE10 PRELIMINARY; PRT; 680 AA.

ID Q9UE10


```

AC Q9UE10;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE KET PROTEIN.
GN KET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKELETAL MUSCLE AND KERATINOCYTE CULTURE;
RX MEDLINE=99018225; PubMed=9799841;
RA Augustin M., Bamberger C., Paul D., Schmale H.;
RT "Cloning and chromosomal mapping of the human p53-related KET gene to
RL chromosome 3q27 and its murine homolog ket to mouse chromosome 16.";
RL Mamm. Genome 9:899-902(1998).
DR EMBL; Y16961; CAA76562.1; -.
DR HSSP; P04637; LYCS.
DR InterPro; IPR001660; -.
DR InterPro; IPR002117; -.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; -.
DR SMART; SM00454; SAM; 1.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;

Query Match          9.3%; Score 186; DB 4; Length 680;
Best Local Similarity 22.2%; Pred. No. 5e-08;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPSWHKESDSEDST-EVDIKEDIPKTVEVSGSELITPEMAFLQGLNGLMQFSQQS 63
   || : ||| : | :|| : | : | :|| : || :
Db 70 QPIDLFVDEPSDGATNKIEISMD--CIRMQSDSL-SDPM-----WPQYTNLG 115
                                         ||:

QY 64 VLREMMLODIQIQ---ANTLPKLENH-----NI 88
   :| | | | | | | :| | | :| | :|
Db 116 LLNSM---DQIQNGSSSTSPTNDHAQNSVTAPSPYAQPSTFDALSPSPAITSNTDYP 172

QY 89 GGYCFSMVLDE---PPKSLMWYSPLNKLKYIRMKAFNVDVQFKSKMPIQLNLRVFLCF 145
   | : | : | : | | | | | | | : | : | : | : | : | : | : | : | : | :
Db 173 GPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM::PPP-QGAVIRAMPVY 231

QY 146 --SNDVSAPVVRCONHLSEVPLFANNAKMRESLLRSENPNSVYAGNAQKGKGISE----RF 199
   : | : | | | | | | | | | | | | | | | | : | : | : | : | : | : |
Db 232 KKAHEVTEVVKRCPNHELRSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 284

QY 200 SVVVPLNMRSRVTRSGLTRQTILAFKFVCQNSCIG---RKETS| *CLEKACGDIVGQHVI 256
   ||:|| : | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 285 SVLVPY---EPQVGTEFTTVLYNFMCNSSCVGMNRRPIL| *LETRDGGQVLGRRCF 340

QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPPEAAEEDEPSK 294
   :|| || ||| || | : || : | : | : | : | : | : | : | : | : | : |
Db 341 EARICACPGDRDKADE--DSIRKQVSDSTKNKGDTK 375

RESULT 15
Q9H3D4
ID Q9H3D4 PRELIMINARY; PRT; 680 AA.
AC Q9H3D4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE TA P63 ALPHA.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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